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⑮ GENE SIGNATURE.

⑮ A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomoly or discriminating cells. The cloned gene can produce porteiins utilizable as a medicine or the like.

EP 0 679 716 A1

Table 4

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: CHUGAI PHARMACEUTICAL CO., LTD.
(B) STREET: 41-8, Takada 3-chrome, Toshima-ku
(C) CITY: Tokyo
(E) COUNTRY: JAPAN
(F) ZIP: 171

(ii) TITLE OF INVENTION: GENE SIGNATURE

(iii) NUMBER OF SEQUENCES: 7848

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 in., DS, 1.44 MB
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/ MS-DOS
(D) SOFTWARE: MS-DOS

(v) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: EP 95900295.7

(vi) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: PCT/JP94/01916
(B) FILING DATE: 11. November 1994

SEQ ID NO:111
SEQUENCE LENGTH:375
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS00124

SEQUENCE DESCRIPTION:

GATCCTACCT ATCAAGCACT AAAAAGTTGA ACCATTATAC TTTATATCTG TAATGATACT 60
GATTATGAAA TGTCCCCTCA AACTCATTGC AGCAGATAAC TTTTGTGAGT CATTGACTTC 120
ATTTTATATT TAAAAAATTA TGGAATATCA TCTGTCATTA TATTCTANTT AANGTTGTGC 180
ATAATGCTTT GGAANAATGG GTCTTTTATA GGAAAAAACC TGGGATAACT GATTTCTATG 240
GCTTTCAAAG CTNAAATATN TAATATACTA AACCANCTCT AATATTGCTT CTTGTGTTTT 300
ACTGTCAGNT TAANTTACAG CTTTATGGG TGGTAACTT TTCGTNCATT TTCAAAAAAN 360
CCNGGGGNNN NNNNN 375

SEQ ID NO:112
SEQUENCE LENGTH:356
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS00125

SEQUENCE DESCRIPTION:

GATCTCTGTT TTGTTGTGA AAATTCATTT GTATACTTTT GTTTTATCT AGGACTTCAT 60
GTTTTTTNAA AGCACTGGCA GCCAGGAACA AAAATCAGGA GTGTGGTAGT GGATTAGTGA 120
AAGTCTCCTC AGGAAATCTG AAGTCTGTAT ATTGATTGAN ACTATCTAAN CTCATACCTG 180
TATGANTTAA GCTGTAAGGC CTGTAGCTCT GGTGTGTATAC TTTTCCTTTT CAAATTATAG 240
TTTATCTNCT GTATAACTGA TTTATAAAGG TTTTGTGACA TTTNTNAATA CTCATTGTCA 300
ATTTGAGAAA AAGGACATAT GAGTTTTTNC ATTTATTAAT GNAACTNCCT TTGAAA 356

SEQ ID NO:113
SEQUENCE LENGTH:351
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS00127

SEQUENCE DESCRIPTION:

GATCACATTA TNATAAATAA ATGAAAAAAT GATTTAATCT GTAATAAACT GGTTTATTGT 60
GCAGTGACTG TAATATACTA GAGTTATAAT AAATTGTTTA CTCTGCCTCA CCAAACACAT 120
GCTAGGATAT AACCCCCAAA ATAAGTATTT AACTTTGCAT TAGGTATAAA GGAGACTGGG 180
TGCTATAATN AGATTATTTT GAGGCAGACA GAGAGCTGTT ATCCTAACTG ATTTAGTATG 240
TTCTGTAATT GAGAAAATGT TCACCAAATN ATACTTTTGA GTGATTTACA TGTACATTTT 300
ATAGGGGACA TGTCTGTGT ATAGCGAATA AATAACTTTT ATAGTATCAC N 351

SEQ ID NO:114
SEQUENCE LENGTH:352
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00128

5 SEQ ID NO:7844
SEQUENCE LENGTH:37
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTCGCTCGCC CATCCTTATA CAGGCTCAGT TTTGTCT 37

10 SEQ ID NO:7845
SEQUENCE LENGTH:37
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
15 TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTCGCTCGCC CATGTATAGG GACAGCATTT CTGAGAG 37

20 SEQ ID NO:7846
SEQUENCE LENGTH:38
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
25 TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

30 SEQ ID NO:7847
SEQUENCE LENGTH:22
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
35 TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CCAGGGTTTT CCCAGTCACG AC 22

40 SEQ ID NO:7848
SEQUENCE LENGTH:22
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
45 TOPOLOGY:linear
SEQUENCE DESCRIPTION:
TCACACAGGA AACAGCTATG AC 22

50 Claims

- 55 1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

2. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

Fig. 1

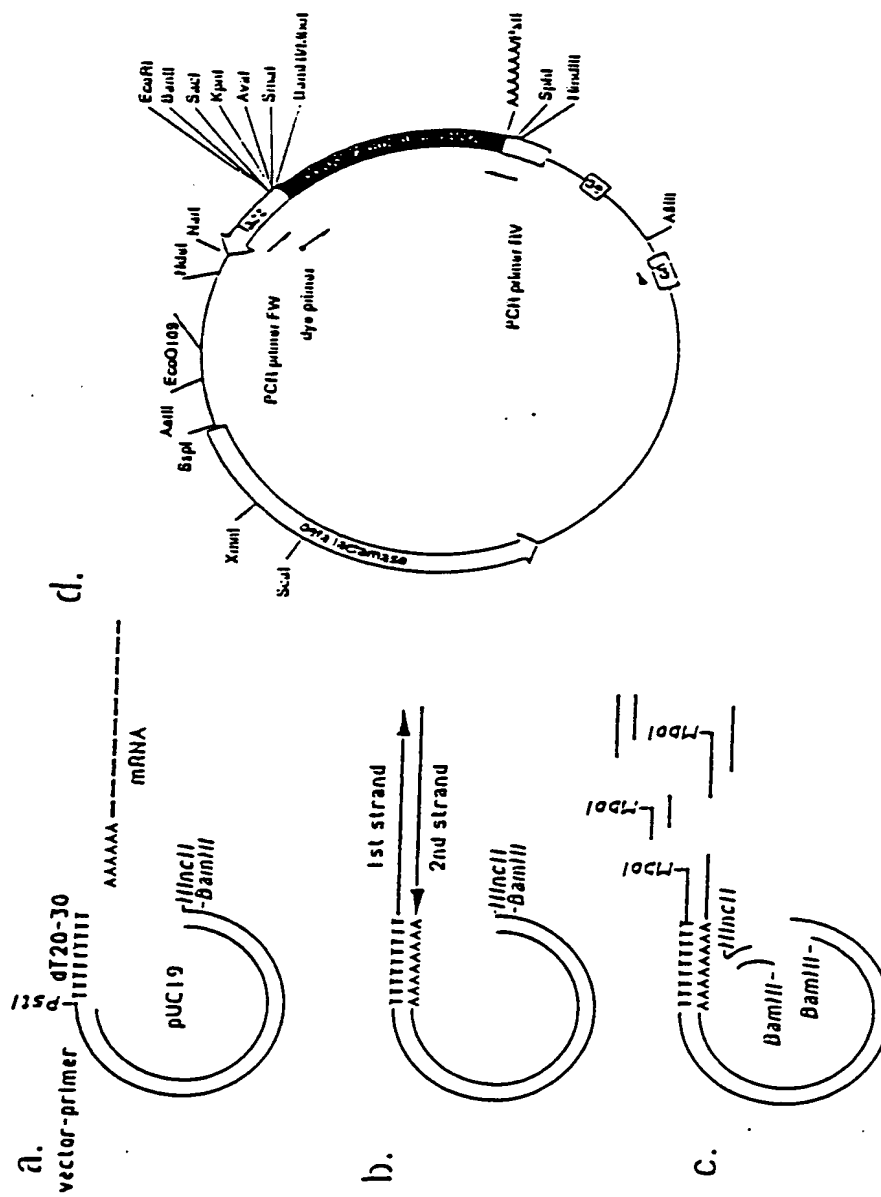


Fig. 2

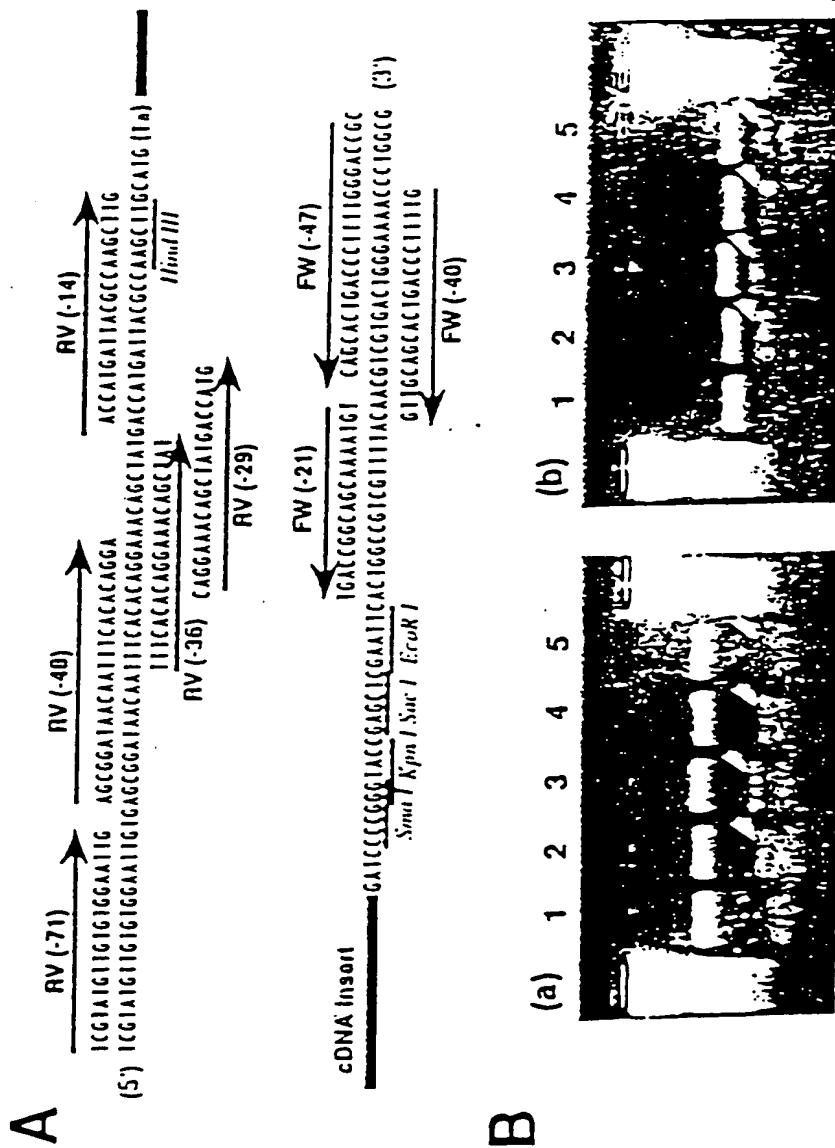


Fig. 3

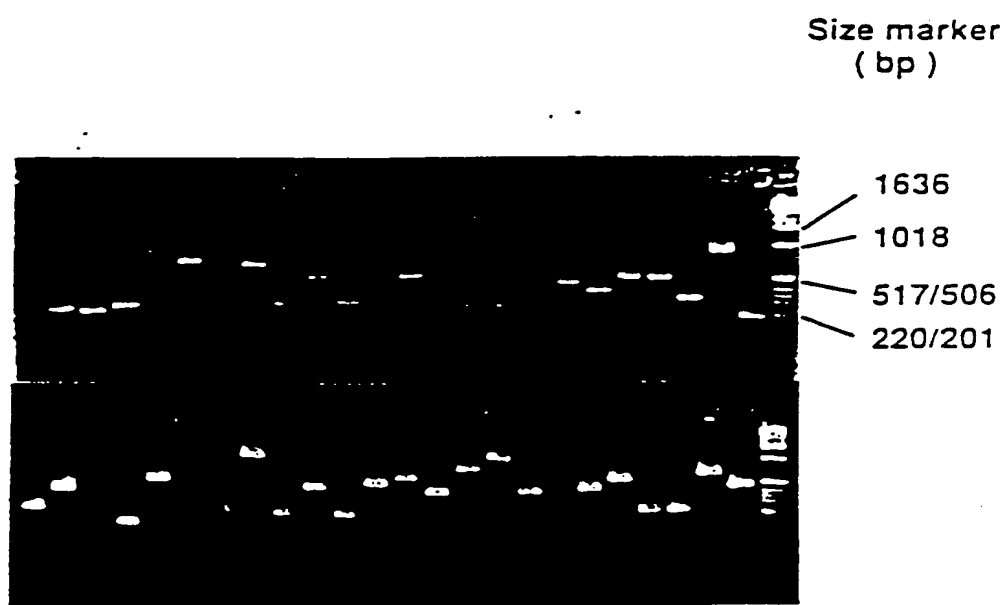


Fig. 4

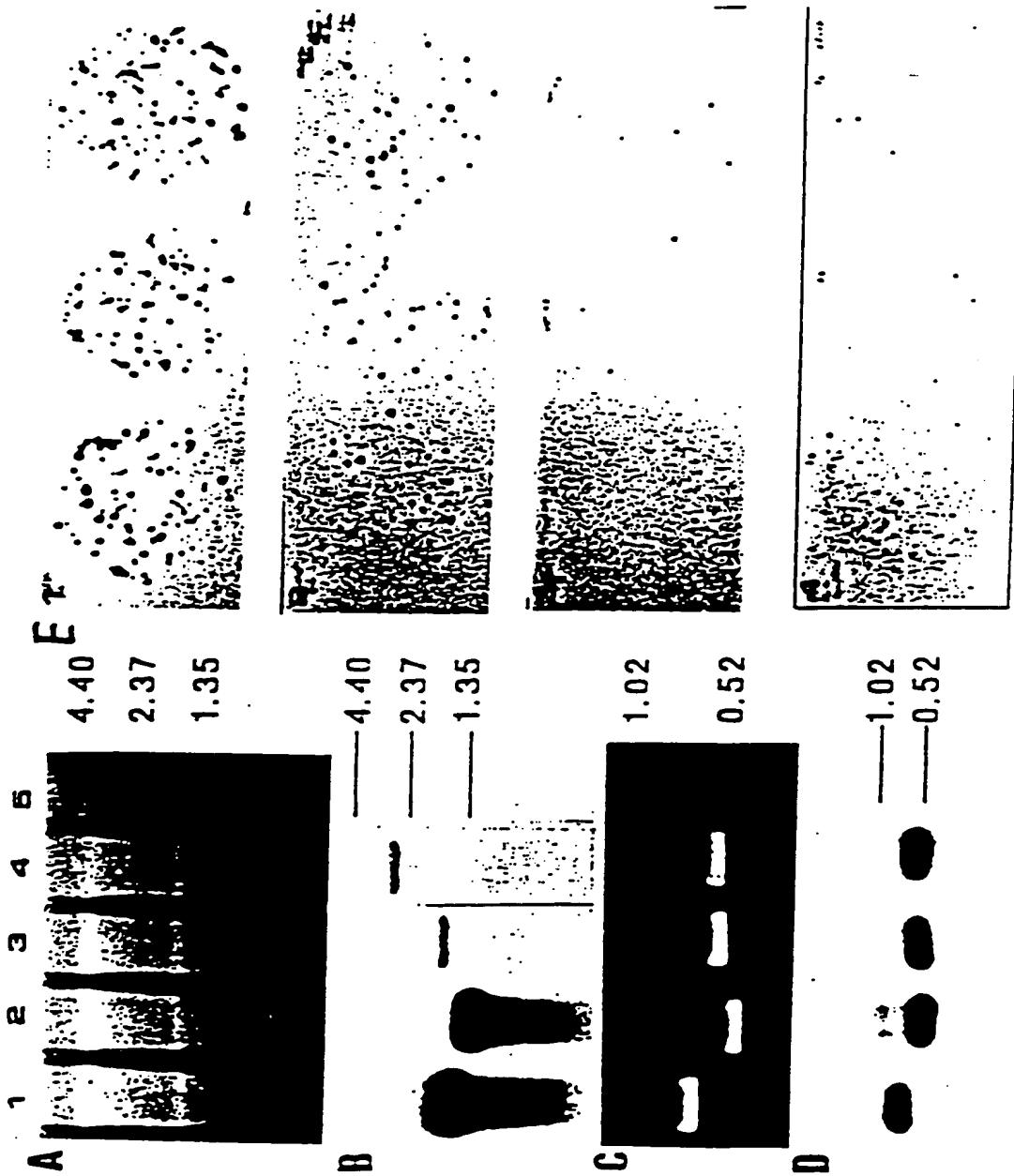


Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1- α	α 1-andrypsin	HnRNP core protein A1	Inter- α -trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b) $\times 10$	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3

Fig. 5

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library

Group	Clone	Gene	A			B			C		
			ln 982 (%)			"in 8,000 (%)"			"in 26,400 (%)"		
I	a15	Elongation factor - 1A α	22 (2.2)			307 (3.5)			NT		
	c321	Translationally restricted tumor protein	12 (1.2)			89 (1.0)			NT		
	ib030	α -1-antitrypsin	8 (0.8)			119 (1.4)			NT		
	hm01b02	Light chain of ferritin	6 (0.6)			62 (0.7)			NT		
	c13a04	NADP(H) Menadione oxidoreductase	4 (0.4)			27 (0.3)			NT		
	hm02d02	Ribosomal protein S11	3 (0.3)			29 (0.3)			NT		
	ib042	Human RNP core protein A1	2 (0.2)			7 (0.1)			NT		
	s155	unknown	1			2			5 (0.02)		
II	s159	unknown	1			2			4 (0.02)		
	s639	unknown	1			1			3 (0.01)		
	s635	unknown	1			0			2 (0.01)		
	s170	unknown	1			0			1 (0.004)		
	s154	unknown	1			0			1 (0.004)		
	s167	unknown	1			0			1 (0.004)		
	s645	unknown	1			0			1 (0.004)		
	s647	unknown	1			0			0 (<0.004)		
	s632	unknown	1			0			0 (<0.004)		

Fig. 6

GS	CII	Chromosomal position	Sequences of primers		AT	IKO	HIE	HIO	CO	G	T
			Sense	Anti-sense							
91600700	pm2166	1	CAGAGCCCCAGTACAACTAT	AAGTTATGTGGGGTCAG	40	114	115	104	110	1	2
91601026	pm2144	1	AATGGGACAGTTACACTGA	CCAGCTTCCTTGACTTGAGA	40	03	04	>200	>200	1	1
91601035	pm2003	1	TGCACTGTGGATACCTATCT	ACAGTACCCCTGAAATGGCT	40	124	124	103	107	4	4
91601607	pm1172	1	GTCACCTTCAGCCATAGCAC	ACCATCTCAGCCACACAT	50	104	104	180	>200	6	6
91601694	pm2347	1	GGCCCTAACAGAGGAACCTC	TAATTCACAGTCCCGTAAC	51	114	116	>200	200	1	1
91601116	pm1771	1	GGGTTTCAATAGGGGTAGACC	GGCCCAATCTGTCAAACTG	48	95	95	70	107	1	1
91601191	pm2609	1	TGGTGGATGTAACTTTTG	GCCGGAACATCAGCTTTTG	47	97	97	200	200	1	1
91601260	pm1251	1	TAAAGAGACCCCTATGGAGACC	AATACTCTGGTTAGTCACITAG	47	97	98	200	200	1	1
91601346	pm2902	1	TCAGGTCTGCTGGAGGATG	AATCAGACAGCAGTATTTG	53	120	122	>200	>200	1	1
91601446	pm1510	1	AAGGTGTACAGGATATTTCAGA	TGCAATAGCCCAATCTCAT	47	130	125	>200	>200	1	1
91601464	pm1438	1	CCAAAGACCTCCGTTGAACA	TTGGGAGAGCCATAGACAG	51	100	100	>200	200	1	1
91601460	pm2427	1	TACTCAGTGGAAAGATAAAC	CAGTGGACCAATTTCTTA	40	90	98	200	200	1	2
91601521	pm2705	1	CCCAAAATCAATTTGTTAAATG	TTTGAATCAGAGACATGAAGTT	43	102,115	100	>200	>200	1	1
91601554	pm1291	1	CCAGAGAGTTCAAGGGATG	GGTACAAGTGGCAATGACT	46	57	57	78	155	1	1
91601572	pm2005	1	CCAACATGTTCCAGCAGCTG	AAACAGTAGTCCCAAGCAT	44	58	55	>200	>200	4	4
91601636	pm1350	2	CATGATACCTTCGGTGGTA	CCCGTTATGGTACATGCT	46	04	109	200	200	1	1
91601650	pm1730	2	AGGCTGAAATGTGGCATGCT	AAACAGTAGTCCCAAGCAT	40	119	119	93	115	1	1
91601659	pm2931	2	AAAGCAATACAAATACCAA	TTCAATATGTTAACCACTA	48	90	90	200	200	1	1
91601713	pm2925	2	TAATGTACCAATGAATAG	TAATGTAAATATGCAGGTAA	45	98	98	200	200	1	1
91601752	pm2935	2	CCAGATGGAAAGGGAAGTCT	CTGGAATATGGAGAAATCAACAG	47	125	125	150	>200	1	1
91601760	pm2093	2	TCAGATTTGTCTCTAATAA	GGAAATATCGCTTCAGTTC	43	103	103	200	200	1	1
91601770	pm2435	2	AGTCCCTTTGGCTCCTCAT	TATCGTCAGTGGCCTTTATG	52	137	137	200	200	1	1
91601777	pm1671	2	TTTGTACCTACGTAAAGTACTT	ATCCGTGCCACACATAGTGA	45	105	108	200	200	1	2
91601785	pm1245	2	TTATAGGGAGTCTATCTCTG	AGTCCCATCTCCACATG	45	67	65	>200	>200	1	2
91601835	pm1246	2	ATCTAGTTTGTGAAGTG	ATGTACAATTTGGGTATGTAGG	45	75	75	170	190	1	1
91601857	pm2440	2	CGAACATTTCACTCTCAT	ACTGATTTGGTCCCATCTG	44	60	67	200	200	1	1
91601881	pm1750	3	TCGGGCTCTTGGTGTGGA	ATGATTTATTTAGGAGGAA	43	60	69	200	200	3	6
91601910	pm2434	3	AAAGAAAGCACACTGGCTAA	GGCCCACTGAGTACAATGTC	51	115	115	200	200	1	1
91601910	pm2660	3	GTAGCTCTGCCCCCTTAGC	ATGTATAGACAATCCAAAG	42	90	90	200	200	1	1
91601977	pm1729	3	GGTCCTTTATTTTQACAT	AAGGATTTGATTTCTTACAT	43	77	77	200	200	1	1
91601986	pm1022	3	GATCCTTGGTGTAGTTCAGTC	AAACAAGAGGATGGTTCAGA	43	75	75	155	>200	1	1
91601990	pm2209	3	ACCCAGTCCCAATCCAGT	CTGCAAAATACAGGAAATCAT	46	83	83	160	160	1	1
91601990	pm2455	3	ATCTAGCTGCTGTAGTAT	ACACTCCCAAGCCCTTACT	55	105	105	113	>200	1	1
91602071	pm1252	4	GTCTTTGCTATCTCTCTTA	TAAAGAGATGAATTTATTTGTT	42	130	130	190	>200	1	1
				AAGCATTTATTTGAGGTTTA	43	90	90	95	>200	1	3

Fig. 7

91000148	pm2256	4	GGCCAGATTCTCTAGTAT	GTCAGTTTATTCAGAGCA	42	62	62	62	69	1	2
91001052	pm1151	4	GTCCATGCACCTGTGTAT	GTCATATATCCATCATCA	43	80	80	-	-	1	1
91001215	pm0988	4	AGAAATTAATAGCATAGT	TAGAGTCMAAGTTCCTGTG	43	100	100	130	-	1	1
91001298	pm1267	4	ATCAAGTTTAAITGCTCA	CATCCATCACAACAGTGC	43	116	116	>200	180	1	1
91000993	pm0901	5	TCCTGTGAAGAGCAGCACAA	TCTAAGGAMGACAGATC	49	101	102	113	200	1	1
91000698	pm1809	5	AGCAATGCCCTTATCCACAG	CTAAGAGCTTGAACCCCTCAT	45	87	87	>200	>200	1	1
91001085	pm0319	5	TACCCAGATAATTACAGT	GAGACATAGCAGGTAAAGT	44	120	120	-	-	1	1
91001101	pm2264	5	ATTTGTACCGTGCTTTAC	AGACAAATATCCCAAAAGC	47	89	89	100	>200	1	1
91001461	pm1160	5	ATTTGTAGTGGTTTACTA	AGAAATGATGCTTTATTC	43	101	99	>200	>200	1	1
91000353	pm2720	6	ATGTGATAGTCTCTTCA	TGCTCCCTCAATGTCTCT	44	78	78	72	>200	2	3
91001226	pm1151	6	CATTGACAGCAGCAGACAG	CTGGCCCTCTCTCTAGTA	53	102	104	145	200	1	1
91001434	pm1216	6	TAGGCAAAACAGGAGAGAG	AAGGAGCTGGTGTGAGGTG	48	65	65	110	>200	1	1
91001457	pm1785	6	TATATGCAATATCCAAAGTCTG	TCTAATATTCGGTCCCTTAICT	46	90	90	>200	>200	1	1
91001523	pm0285	6	TTGTAACTGTGCTGCTAGT	TTTAAATGTGATGTTAT	42	86	70	>200	100	1	1
91001525	pm0228	6	GCACCTAGCCCTCCAAAGT	TATATATCAGTCCAGAGC	49	138	138	>200	>200	1	1
91001562	pm2619	6	TCTGCATTGACAGGAGCCAC	TTTGAGATTTAATGAGTCATG	43	62	62	>200	45	1	1
91000624	pm0991	7	GACCTGAAGTGTGAATGAGT	AACTAGCTTATGGGATTT	45	119	119	>200	-	1	2
91001145	pm0281	7	AGCCAACTCGGGGTGATCT	CCACGGACAGGTGAGTCAT	56	159	159	115	>200	4	4
91001469	pm1101	7	AATCATTTGGGAGAGCTGTA	AAGACAAGTTTATCCAGACA	45	88	89	130	-	1	1
91001578	pm0219	7	TCAGGCAGTCTGCTCAGATA	TTTGCAGTTAATCTGTTA	44	77	76	170	-	1	1
91001207	pm0956	8	AACAGTATGCTGTGTCAGACTAG	TCCATTAATAGCCAGTCTCAG	47	81	81	105	70	1	1
91001176	pm2527	8	TTGCCCTAATGTTGTTCTAC	AAACCAAGAACACACTAAG	48	93	93	118	180	1	1
91001248	pm2708	9	TGTATTGGATTGGATCTG	CAAAAGCAAAACAGCAGATA	44	95	95	-	85	1	1
91001655	pm0995	9	TTGCCATCAAAACACATACA	CTTGTGAGTTTGGTTTCTG	43	55	55	-	-	1	1
91001157	pm0859	9	TTAAGAAATCACCCCTCATTG	CACATGCTTATGGAACT	44	74	74	72	73	1	1
91001268	pm0547	10	AAGTATGTGCAAGAGATGTA	AAGAAACACTGCTTGTGG	45	138	139	>200	>200	2	3
91002278	pm2245	10	TGTAAATGCTATCTCTCT	GCATGCTTCCATATCAGT	47	100	100	200	>200	1	1
91001159	pm2664	11	ATCAAAACAAACAAATCCAGA	AGTATAATATCTGCAACT	42	117	121	134	95	2	2
91001315	pm0880	11	GAATAGCTGGAGATTTCAC	GGAGATCATACCTTCAGCA	46	100	100	84	95	1	1
91001352	pm0445	11	AAAGTACCTTGTGACAGTGGGA	TGAGCCMAAATACATGCTGACT	50	153	153	>200	160	1	2
91001489	pm2943	11	AGGGTGAAGGGTATTTTACG	CACATCAGTTGTAGAGCTA	47	83	85	-	-	2	2
91001570	pm2810	11	AACCCCTAGTAAGGCATTG	TTATTAACCAATCCAGTA	37	47	47	125	53	1	1
91000279	pm2666	11	CTGTAAAGGTTTTGGAAATATGT	TTTCAATTTTCTACCAATTAIT	42	75,82	75	145	>200	3	3
91001163	pm2756	12	AGTGTATGGAAGACCTTGAG	GTTCAATTGAAACGGGTAGC	48	130	130	103	>200	1	2
91001193	pm1193	12	TCTCCCTATTCACAAAGT	AATGATTCTGAGGATAGCA	49	88	89	>200	120	1	2
91001235	pm2790	12	CACAGATAAAGAAATCATA	ACCCTAATTTAGTTTCTCAG	46	100	100	-	-	1	1
91001274	pm1355	12	CATCATGGTACAGTCAGAG	CAGTTGTCAAAATGTAITG	44	83	82	91	87	1	1
91001208	pm1355	12	AGATGCTAGTATTTCTCTCATGG	DAGAACAGCAGTAAGCAACCAC	47	87	87	>200	>200	1	1
91001308	pm0368	12	CCAAAGTGTAGGGTACAG	TTCAATAGACCTTGGTTAC	47	95,165	95	>200	>200	1	1
91000159	pm2845	13	CTAAGATTAAATGCGATTC	AGTAGTGTATGCGAGAGGA	46	104	104	>200	>200	1	2

Fig. 8

91.001014	pm1658	13	TTGTAAGCCTATCAGAGTCA	AGCAGAGCTATGCCATCTA	44	109,200	109	>200	100	1
91.001290	pm1721	13	GCCTCTCCGCTGCTGTGGT	GCAGTTAATCAGGCTATCTCC	50	122	122	>200	130	1
91.001262	pm1710	13	ACTGAATGGAACTAGTCT	TACATTAATCAGCATGTGA	40	61	61	95	101	1
91.001366	pm1364	13	TGCTTAGCTTCCCTCTTA	GAGCATTTCTGTTCTGA	45	67	67	-	-	1
91.001309	pm2301	13	CATGAACCTGCTCAGACAA	GCTTACTTTATGCTGACC	51	100	100	100, >200	-	1
91.001402	pm1541	13	AAATGAATGTAATAGCACT	ATTAGTTTACAGGGAGAAT	41	72	72	-	74	1
91.001367	pm1411	14	GTTTAAAGTTTGAATTGGG	CATCCACCTACATTTCT	41	77	77	>200	100	3
91.001564	pm2307	14	CGTTCCTAACTCGAAATC	AATGCTATTATCTCAAG	42	55	55	>200	>200	1
91.001576	pm2010	14	ATCACAATTACCTTTAGTGT	ACGATACTTTATGAGAT	39	69	69	-	-	1
91.001330	pm2720	15	TCCCATCCTCAGTTGAAT	TGAGAACAAAGGAACCACT	47	70	70	00	150	1
91.000960	pm1915	10	TTGGAAATGGAACCTTGCTA	ACTTATGCTGCCGAAATGG	48	79	79	66	70	2
91.001242	pm1127	16	CCCTTGTTTACATGTCA	TATTAATCTGCCATTCAT	44	105	105	103	102	2
91.001516	pm2543	16	ACAGTCTTAAATCAAAGGTG	TCTGACACTCAAGTGGCAAT	45	70	70	>200	-	1
91.001566	pm10913	16	TTTGTCGGACTATGTAAT	TCACTTTATGGGAACCAAG	41	53	53	>200	>200	1
91.000206	pm1157	17	CTCTCCATGTTCTACAAAG	TAGAAGGAGAACTCTGTGTT	47	77	77	140	>200	2
91.001015	pm2360	17	ATATTCACCTTCCCATCCAT	TCAAATACGTCCTCTCAAGC	50	80	80	>200	>200	1
91.001156	pm202	17	CAGAAATTAAGTGCAGCAAT	TCGATCTGCATCTTAAAT	45	103	100	>200	>200	2
91.001173	pm2117	17	AAATCTGTGGTTATTTCC	GTGATCTGCTGACATGTC	41	110	118	145	200	1
91.001301	pm1070	17	TAAATTTGGAAATCTCTGGA	ACACATTTGGGTTGCTTTAAC	47	100	100	95	97	1
91.001316	pm10511	17	TGTGACAGCAGCAGCTCAT	TCGTACATTTAATCTCCACC	45	120	129	-	-	1
91.001256	pm10530	17	CATCTCAGACAAAGGAAC	ACCTAAGATCCAGAGAAAC	40	90	90	69	>200	1
91.001405	pm2212	17	TGACIGCAATAGGAGTTGT	GAACATACCACGTTATTCT	46	90	90	180	>200	1
91.001522	pm10642	17	GTCTCAGCAGATTACAGTT	ACTTCTCTTGAGGACACA	45	68	68	160	-	1
91.001070	pm1015	18	TGTTCTCTCCAGCTTGTAG	GTTACATGCTTGGTACAG	49	65	65	>200	>200	1
91.001117	pm2309	19	GGATCAGACCAACAGTGTCTG	GCAAGGTATAAACAGATTGA	46	50	50	-	-	1
91.001467	pm1690	19	GAAGCCCAACCTGCACCTCA	GGAGAGTATGGGGAACGGT	54	93	93	>200	>200	2
91.001069	pm1079	20	GCCATGCTTTAAAGTGAATGT	TTAAGAAGCATTAGCTAGGATA	48	140	140	-	-	1
91.001000	pm1146	20	GCCCTAGGATTCACTGCTC	ACCACCAAGTCTTTCAGG	52	66	66	180	>200	1
91.001069	pm1112	20	TGCTGGATGACTCTACACG	TCCCTATCATGGCTGCTGTT	49	59	59	59, 115	59	1
91.001120	pm10332	20	CTGCTGGCTAGTCTGACTC	CAMAAGTCTAAGAGACAT	49	135	135	153	160	1
91.001132	pm10647	20	TCTGAATGATGATGGAACA	ATCCTAGTCCCAACCCAGTA	48	109	109	-	-	1
91.001150	pm1774	20	GGAGCCACATGGATTGATTG	AAATGTACCCCTGGCACCTC	52	124	124	>200	>200	1
91.001210	pm1235	20	AGCCATCGGTTATGCTTA	GGAGCAGAAATGAACCTTAC	44	90	90	>200	>200	1
91.001295	pm2101	20	TCCATGGTGTAGAAGCCAG	CCACATCTCCACAGGGAGT	54	142	142	>200	74	1
91.001427	pm10640	21	CTCTGCTATAAAGTAGAG	TTTATAGTCCACACAGAGT	45	130	130	180	>200	1
91.000970	pm10912	21	GGTGTAGTGAACCAATTAG	ACAATGGTTCCTAAATGA	39	50	50	145	>200	1
91.001444	pm10911	22	GGTCTGTCTCCCATCTGT	AGTTGCACCATCTCTGTC	46	124	124	>200	>200	1
91.001473	pm12231	22	TGAGCTGCATCTACCTGTGAGG	AGAAAGCCCAAGTAGTCC	48	65, 80	65	100	125	1
91.001479	pm12320	22	TACAGCCCTCCCAAGCTAAAC	AAGCAGGTGAGTTGGGTTTCT	50	94	94	67	135	2
		22		TTTATCTGCACTCCACTACAA	46	65	65	190	>200	1

Fig. 9

91000999	pin1759	X	CTCCATAGTTACCTGGATT	TCACCCACCACTATTAGCA	47	103	103	-	-	1
91001119	pin2160	X	GGAGGGAGATAGATTGT	AAAAATCCAGAGACTGA	46	70	70	135	130	1
91001161	pin0608	X	TTCATTAAGTGTGACCGTT	GGAGGATTGAGATACAT	40	85	85	>200	77	1
91001104	pin1291	X	TATGCCAGTGAATGTTCGTAA	GTAAGGTTATCTTGCATCAGA	47	02	02	>200	80	2
91001168	pin2289	1,10	ATCCTGCTGAATACATCTG	GGGGAGAGACATCACATGAC	46	70	70	68	130	1
91001136	pin0113	1,2,12,13,Y	GATCCGATGAGAGTGAAT	AATACAGCTAACCCCAA	44	69	69	170	-	1
91001104	pin2272	1,2,3,5,8,12,14,17,X	TTCGATTCACATCTCTAT	TTCATGTACAAAGCACT	43	130	130	150	132	2
91000303	pin0314	1,2,6,X	TATCAGCTGAATATGTCAC	TTACTGAATCCAGCCAACA	45	93	93	110	-	1
91001140	pin1481	1,3,4,5,8,10	TCCMATGAAGAGGTGTA	AGTTGACAGCCAGGTGAATG	43	96	96	100	100	1
91001351	pin1561	2,20,21,22	GTCTGTCAAGCCAGATTCA	TTTTTATGTGCTCCAAGT	43	110	110	170	150	1
91000376	pin2795	2,4,5,10,12,15,17,20,22,Y	GACCTGTGACATCTGGACT	TTATAGGTGTACACTCG	43	61	61	-	-	2
91001077	pin0913	2,5,14,C	GCCTGTGATTCACCCTG	ATCTCCCTTGCTCCAGTTA	46	82	82	>200	82	1
91001192	pin1653	2,8,12	TCTGAGGACATCCAGACAG	CAGTCAAAACCAACACGGTAT	49	95	95	93	160	1
91000213	pin1778	2,9,13,17,X	TGCATTAAGGGGAAGACCA	CCGTTGAGGTGATGAATG	49	78	80	>200	>200	1
91000919	pin0885	20,X	GTCAATTGTATGCAATTTC	ACATTTATTTTTCACCG	37	45	45	-	-	1
91001109	pin0457	3,10,15	CATGTACTCAGAGGCATTC	GCACCTACAAATCCCAACT	50	133	133	>200	150	2
91000071	pin2651	3,4,11	CAGGACTGGAGCAGGAAG	GATTTACCATTAGGAAGC	50	101	101	101	88	3
91001126	pin2632	3,6	TTAGGAAATATGTTAGACAG	ATAGTATGGGTGACACAGTA	43	80	80	>200	120	1
91001191	pin1133	3,8	TGGATTGCTTACCTGTT	ACACCTCAGGAGATGTTAC	47	91	93	95	>200	1
91000377	pin2250	3,9,10,15	GCACACAAGCCAAATCAGA	CTCTTACACCAACACAGCAG	50	96	96	>200	135	2
91000603	pin0626	4,6	GGATTCTCTGTGTCAT	GTTTATGTACGGCATTTAC	44	105	100	>200	>200	2
91001212	pin1231	6,20	GCATTAACAGGAAACAATA	CTGTCCATGTGCGATAACG	44	110	110	105	107	1
91001312	pin0606	7,18	AGATGCTACATTAGGGATA	TTTACGACATACAGAGAGT	43	81	81	102	-	1
91001111	pin1253	9,11	CCAGACTACAGGCTGATGGC	CCCTTACCCCAAGCACTCTT	55	75,130	75	>200	>200	1
91001357	pin0115	9,11	ACCAATGTCACCTGCTTAATA	CCCATAAAGTGAAGAGTACTTC	48	125,155	127	125	>200	1
91001261	pin0128	10,15,22	AAGAAATGTTTACTGGATT	TTATCTGACTTGGAGGAAT	42	107	107	-	-	1
91001154	pin2120	10,15,22	ACTACCCCTGAGATATAGTT	TTCATTTATTTATAGTTGA	46	100	100	170	-	1
91000750	pin2303	11,11	ATACCACTCCGCTGTACCG	GAGGAGCTCTACTGGTCTT	50	72	74	72	>200	3
91000314	pin2613	12,19	GCACCAAGAGCAGTCCAG	TTGGGAATGAGAAAATAACT	46	83	83	81	-	1
91001003	pin2273	12,11	GATCTCAGTCTGCGTTATT	TACATACAAAGATGCCAACAGT	44	80	80	79	68	1
91001187	pin2725	13,16	ATCTGTGTGCTGCTTCC	GTCTCTCTCTGATGGCTGA	46	62	60	135	180	1
91000976	pin2780	14,16	AACCTGTTTACCGCATCTT	AGGTATTGTTCACCAAGAA	48	87	87	>200	>200	1
91001135	pin1683	17,20,C	TGTGGTTCACCATTGAGAC	AGACACACATCAAAAGATGC	46	90	90	>200	00	1
91001193	pin1740	17,22,Y	GAAATGATCCCAAGAGCTAG	CTAGTTATCTCTGGCTCTG	44	81	81	>200	200	1
91000566	pin0564	17,C	TTTATCCCAAGCAGCAGAAC	TCTCTCTCTCTCTCTCTCTC	40	120	120	>200	170	4
91001369	pin2217	17,C	ACTTAAGTAGCTTTGTACG	TGCCCTCTGCTCTGATAATA	43	95	95	>200	95	1
91001140	pin1213	18,C	CCCCAGTTAAGGATATGTT	AGTGACGATGGAGGAGTGA	44	92	92	-	92	1
91001217	pin1118	19,20	TGCAGAGTGATTTTCCAGAG	CGTAGGCTATCTTTCAGC	46	75	72	160	65	1
91001009	pin2824	19,22	ATCCCTGTCTATTCACAC	GCCTGTTAACCTCATCTCAC	46	110	110	130	170	2
91001172	pin0887	19,22	GCCTGCATCTGTGTGACTT	AACCTCTGGGAACAAATCAT	48	91	89	160	86	1

Fig. 10

g1001057	pin2040	C	AGSACAAACACACAGCTAT	TTTTCTGATTATGACATGAC	45	75	75	101	75	1	1
g1000173	pin1353	N	ATCTCTTTAGCCATCTG	GTAAAGTGTGATGCCATT	42	64,100	64	64	>200	1	1
g1001096	pin2230	N	GTAGAGCTGCATTGACCTG	ACAGACAAGGAATAATCATG	42	100,96	110	110	112	1	1
g1001166	pin0506	N	GTCCACAGTCCAGCTAAC	GCCACATATAGAAATCCATC	46	74	74	74	>200	1	1
g1001151	pin2351	N	TGCTTTGTGACTCTGCT	TTTAAACAGTCAATAATACATGTT	46	110	110	110	106	1	1
g1000270	pin2402	M,C	GCTAGAAAGAGGGCACTCA	CTTAACCTGATAGCCAGGTC	44	75	75	75	75	1	1
g1000253	pin2706	M,C	CACAAAACAGCAACTTCAG	ATGGTTATTTATCAATTC	41	83	83	82	81	2	3
g1000265	pin1704	M,C	TCCACCACAGAGAGCACACT	AATTCATAGGGAATAGGTC	40	75,130	75	75	75	1	23
g1000302	pin2310	M,C	TGCAGAGGACCAAAATCAC	GAACAGGTTAGTCCATTCG	40	50	50	58	50	1	1
g1000513	pin1609	M,C	CATGAGGCTACGAAACAGG	AGGAGTCCGTGGGTCTGAG	51	81	81	84	84	4	18
g1000575	pin1442	M,C	AAAGCATCTGAGAGGAACA	GGAGGACTCGCTTGGCTCTTA	49	110, >200	110	110	110	1	8
g1000732	pin1452	M,C	GCAGCAGATACCTTACACC	TGGTTTCATTTCAGTTCCTTC	51	102	105	102	102	3	13
g1000995	pin0760	M,C	GAGCTCTGTGAGGAAAGT	CAGACCCATCTTTATACC	47	79	79	79	79	3	4
g1001016	pin2783	M,C	ACGATATTTATAGTAGTG	TCAAACTTTAATATATGCT	40	83	83	91	92	1	1
g1001053	pin1144	M,C	AGATGAGTGTGGTTCAGAGA	CCATTCCTGATTCAGTTC	52	135	140	135	135	1	1
g1001127	pin2290	M,C	ACTGTRATGGAAGATACCA	CCACACAGTACGACCCGCT	47	55	55	55	55	1	1
g1001167	pin1626	M,C	GAGAGCCCTTCATCCCTTA	CTCCCTTGGTCTTCTGCT	49	100	100	100	100	1	1
g1001216	pin2108	M,C	TAAGTCAGAGATCAGTAAGT	ACATGTTATTTAATATCTT	42	110	110	110	110	1	2
g1001353	pin1240	M,C	AACTGGTCCATCAAGACTG	AGTGAATAAACTCTCCATCC	48	120	120	120	120	1	1
g1001321	pin1131	M,C	ACTTAAAAACCCACACGAT	ACAAACAGCAGTCAAAATAGAA	47	87	87	87	87	1	1
g1001375	pin0952	M,C	AAGAGGAGTTCCCTGCTCA	ATCATGACAGATGCCAAGGA	51	89	89	89	150	1	1
g1001356	pin2216	M,C	ATCTGCATGAGCTATATCT	CGTCTCTTTTATTTGACAT	45	100	100	100	100	1	1
g1001411	pin0950	M,C	ATGGGTTATCAGGGGTTTC	CAGACCAAGGACACTCTTA	47	80	77	80	80	1	1
g1001460	pin2026	M,C	ACATTTGAATGGGATGAGGT	GGACATTTCTAGCCACAGC	51	75,55	75	75	75	1	2
g1001402	pin1210	M,C	TTGTTGACATTCCTTTTAGAA	CAGTCCCTCTGACTGAGACA	48	85	85	85	85	1	2
g1001450	pin0100	M,C	GCCCACAGACATCATCCT	TCTTAGTAGGTGCTCTGGTG	51	90	90	90	90	1	1
g1000510	pin2042	No product	CAACCAATAGGCTGAAAGT	GAAATACTCTGTCATCTA	45	87	87	87	87	1	1
g1000550	pin0304	No product	CTTTGGGATATTTCTTCAT	CCCTCGGGTACTTTCTATG	43	60	60	62	62	1	2
g1000561	pin0800	No product	AGCCAGCCTCTTGTATGTG	CTGGATTGATTTTCATAG	44	87	87	87	112	1	1
g1001354	pin1073	No product	TGTGGTATGAAATATCTGA	TTATGAATGAGACAACACT	43	98	98	103	>200	1	1
g1001365	pin2900	No product	CAGTAGTGTGCTTTGAAATG	TTATGTAATGTTGGTGT	41	63	63	63	150	3	3
g1001373	pin0361	No product	TACAGCCGCTCTAAAGTC	TTTACGATCAAGGAAATCT	48	82	82	82	>200	1	1
g1001556	pin0049	No product	TACATTCCTCAGACTCATG	TTTCAAAACTTTATCTT	40	86	86	86	>200	1	1
g1001574	pin1284	No product	ATCAGAGCTCAGTCTCTAG	ATTTCCTCTGCTATGGTC	44	57	57	57	67	2	2
g1001622	pin1606	No product	GATCTTGAGCCTTAACGGA	TTTCCAGTTCAGCTTTATTC	45	54	54	54	54	1	1
g1001640	pin0952	No product	GATCTCTGTTCTTTTCA	TTTATACAGACACCACTAC	36	45	45	45	45	1	1

Fig. 11

pm2209 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y H H C N

Fig. 12

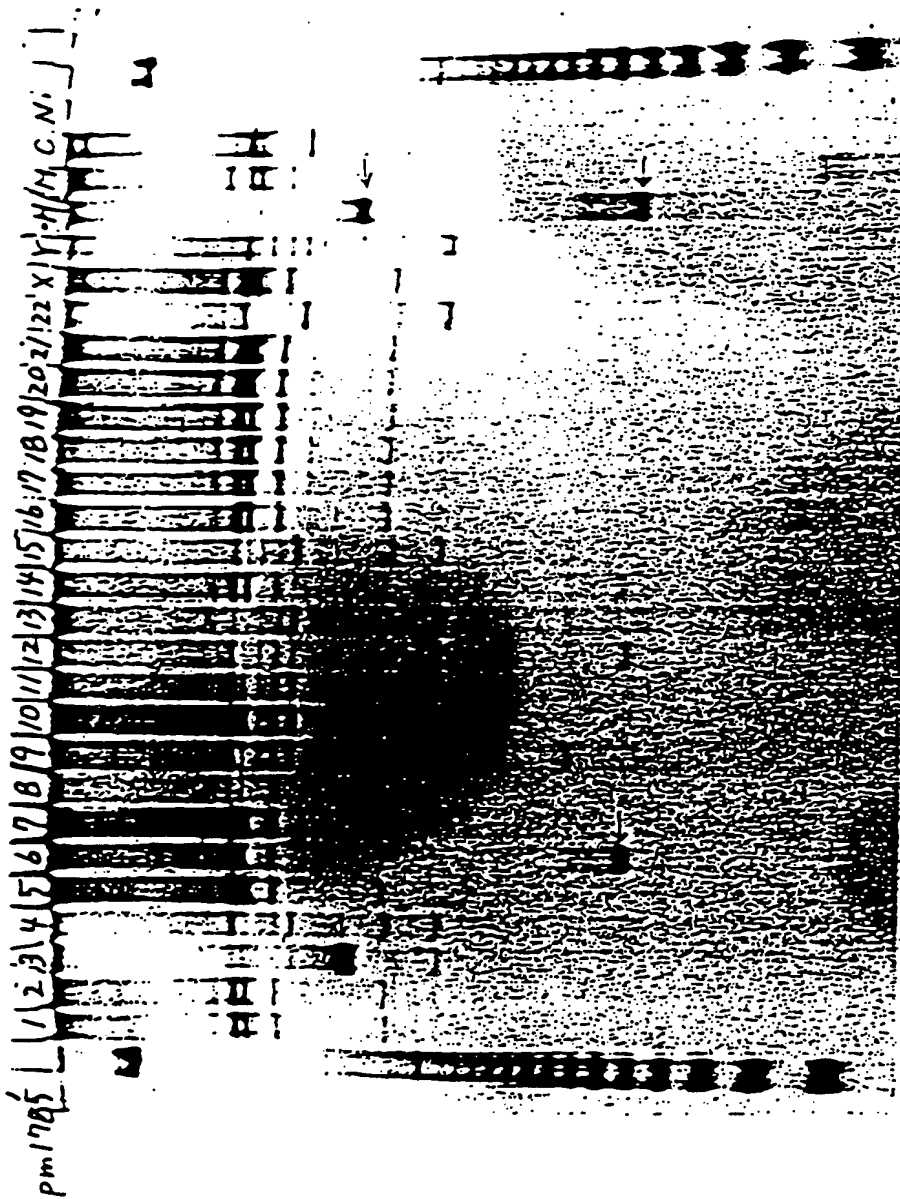


Fig. 13

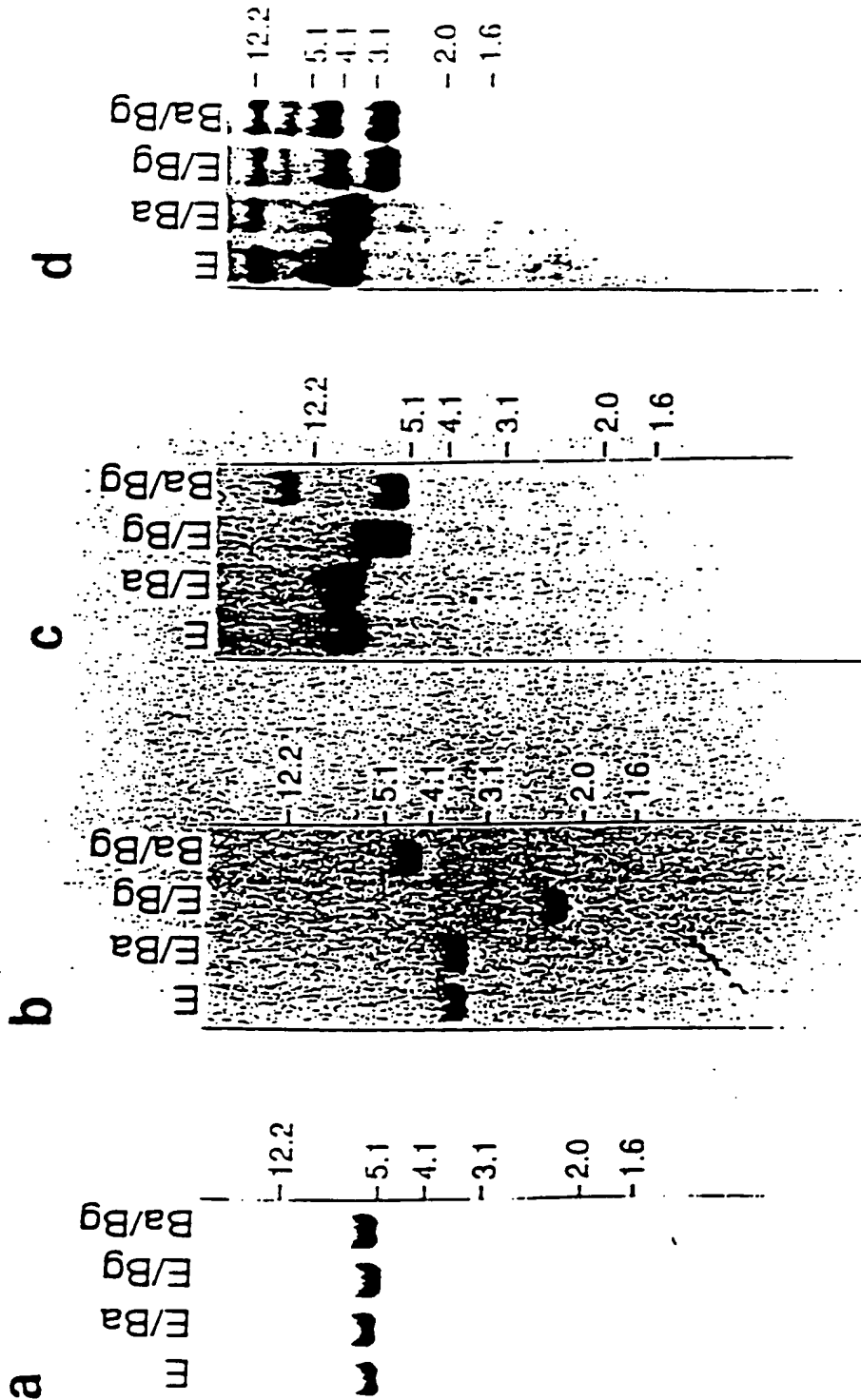


Fig. 14

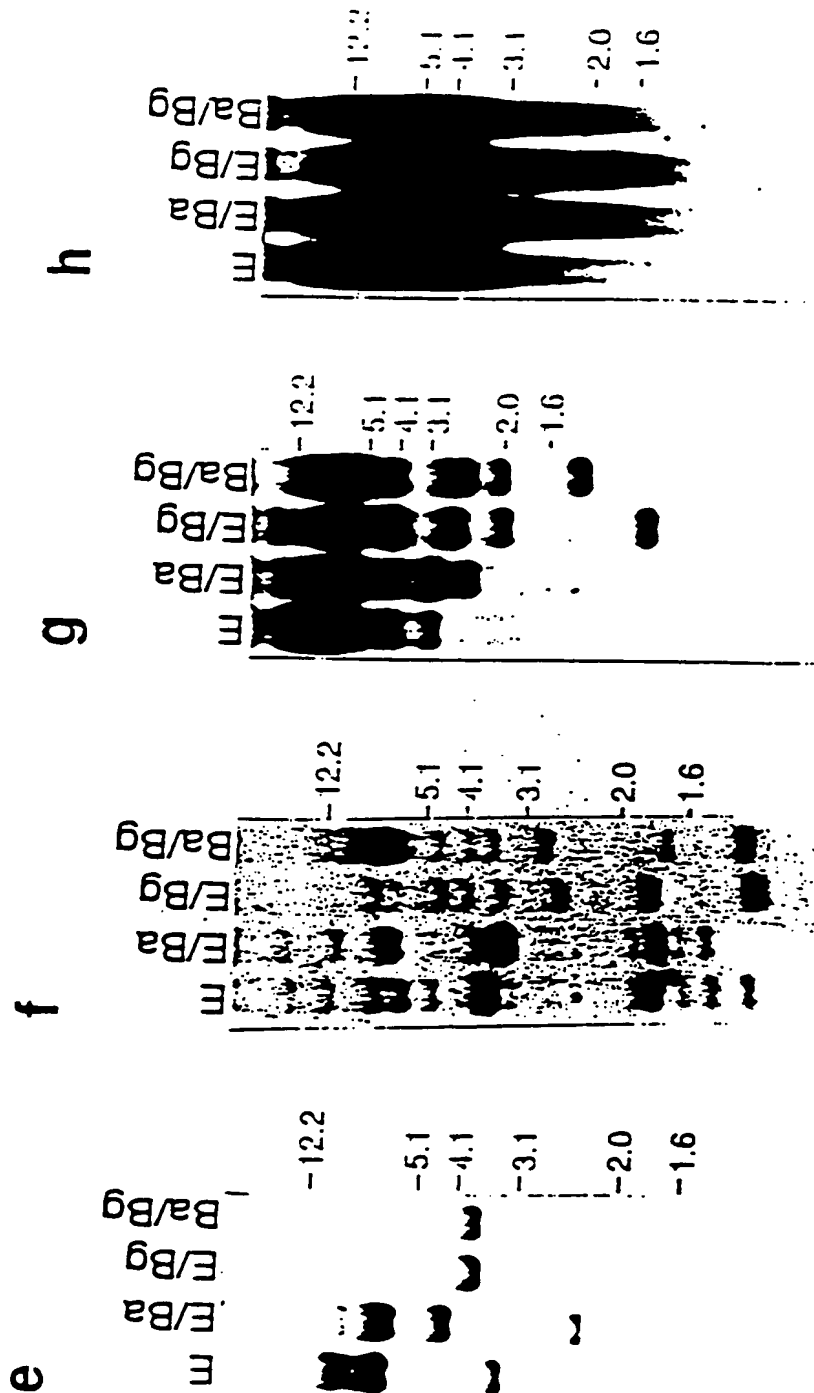


Fig. 15

Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (3)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	73
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10498	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9

Fig. 16

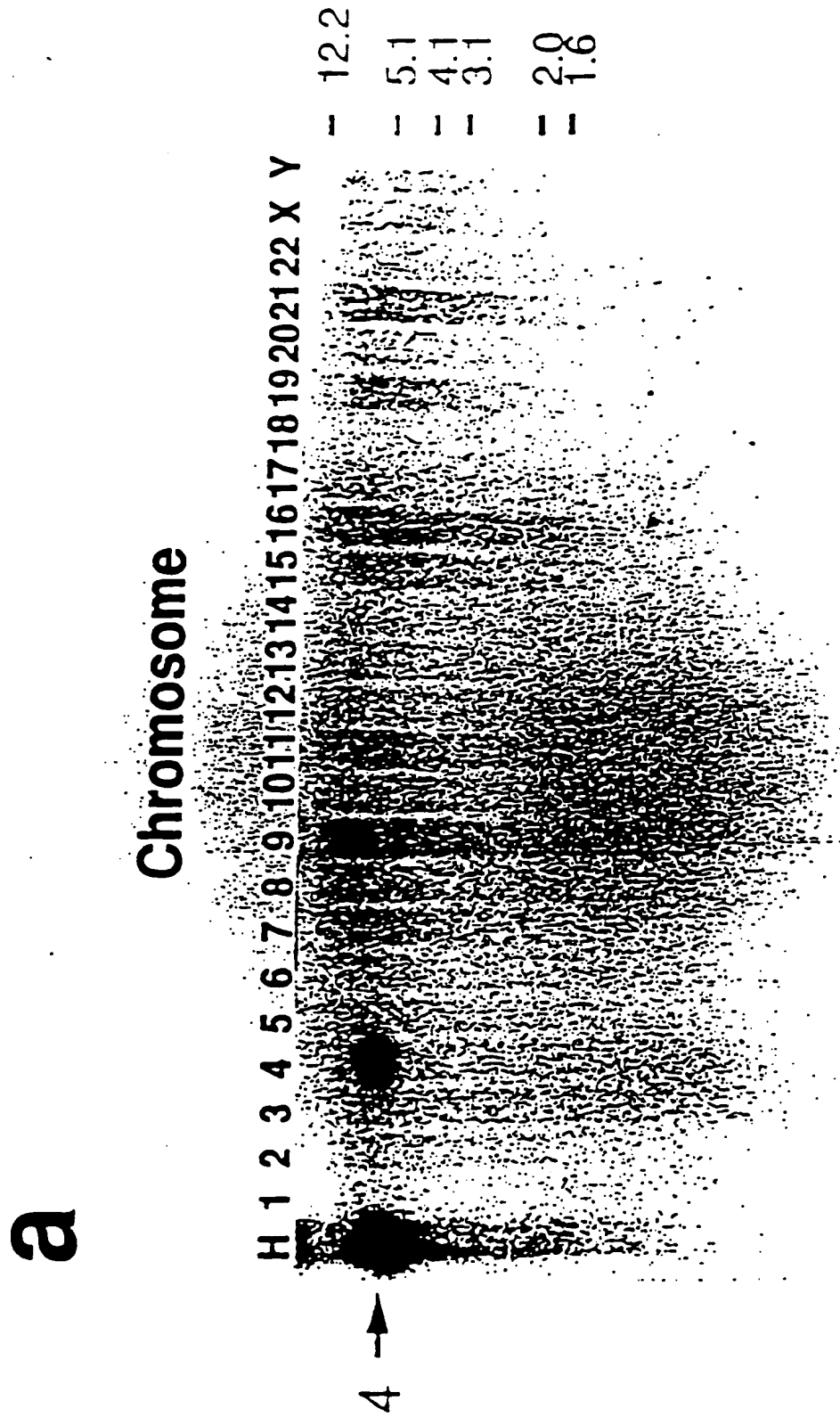


Fig. 17

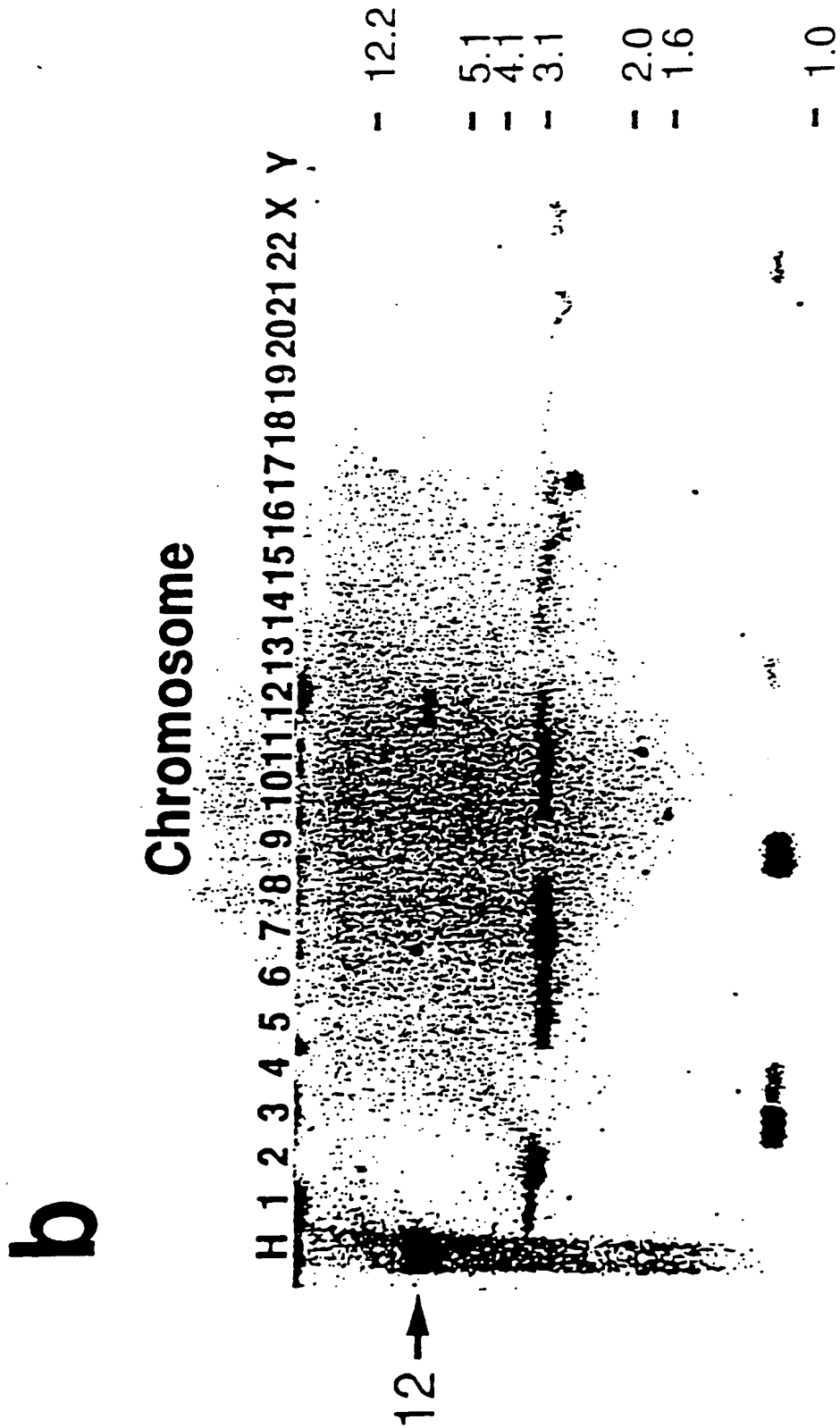


Fig. 18

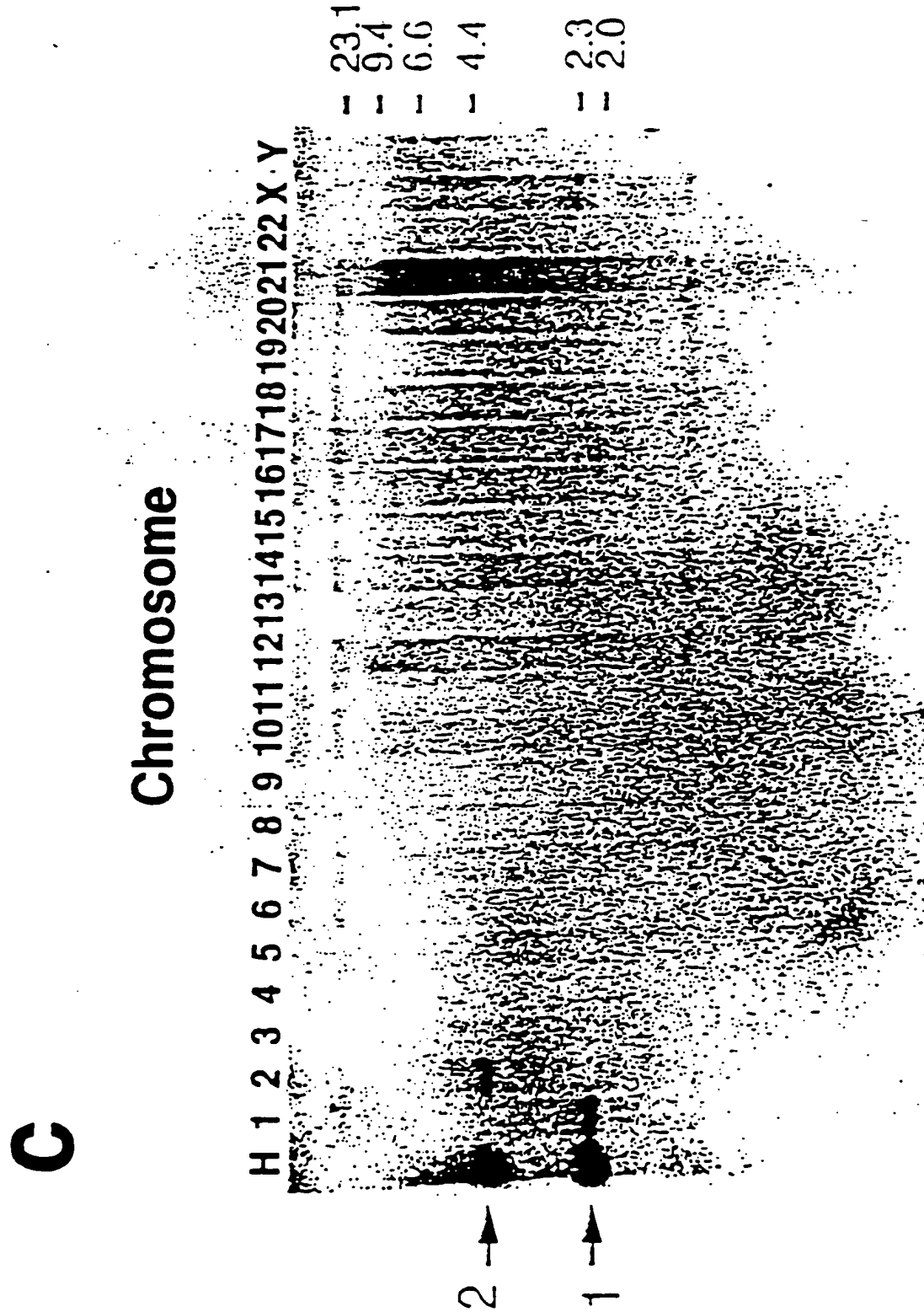


Fig. 19

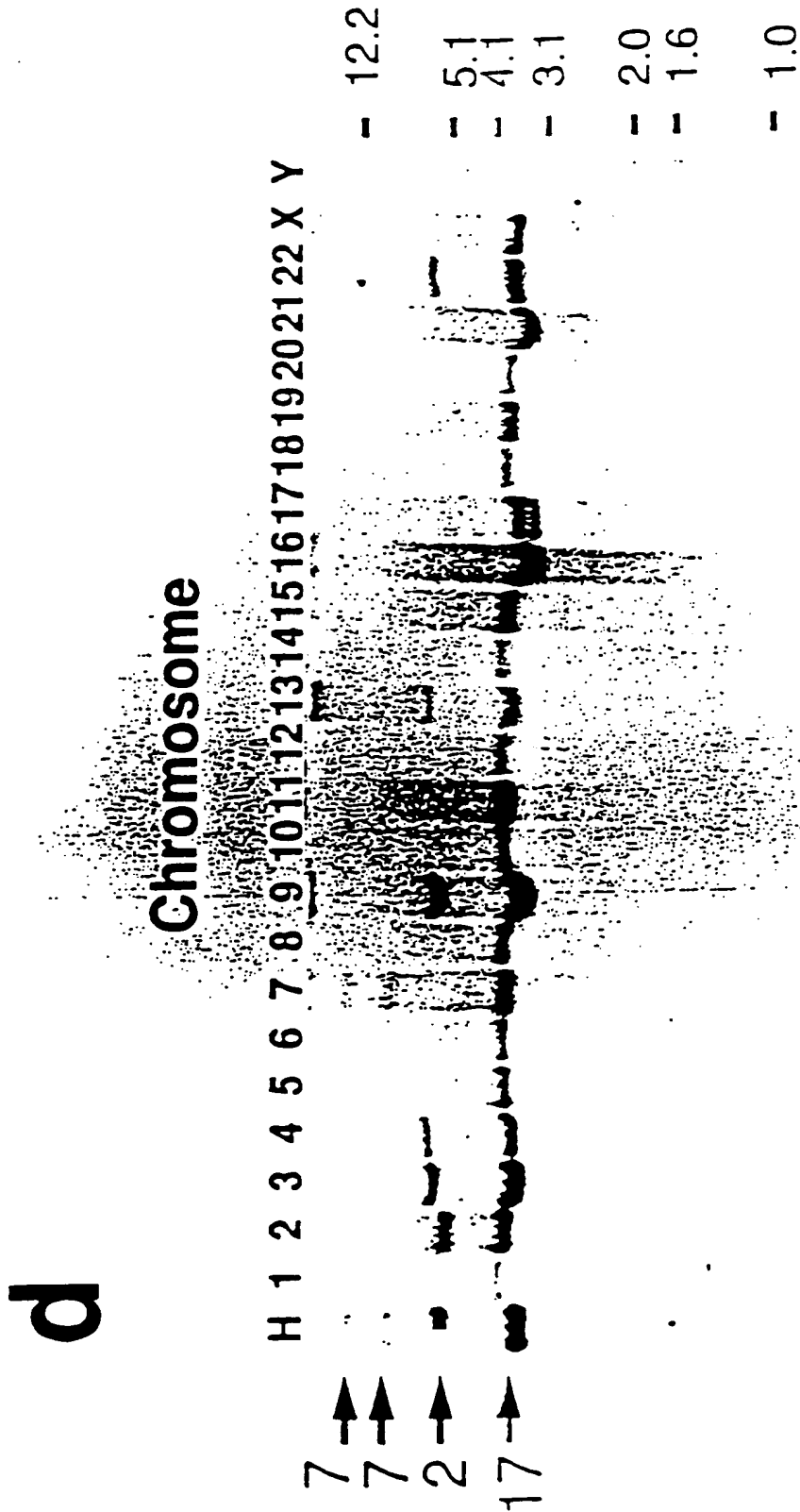


Fig. 20

e

Chromosome

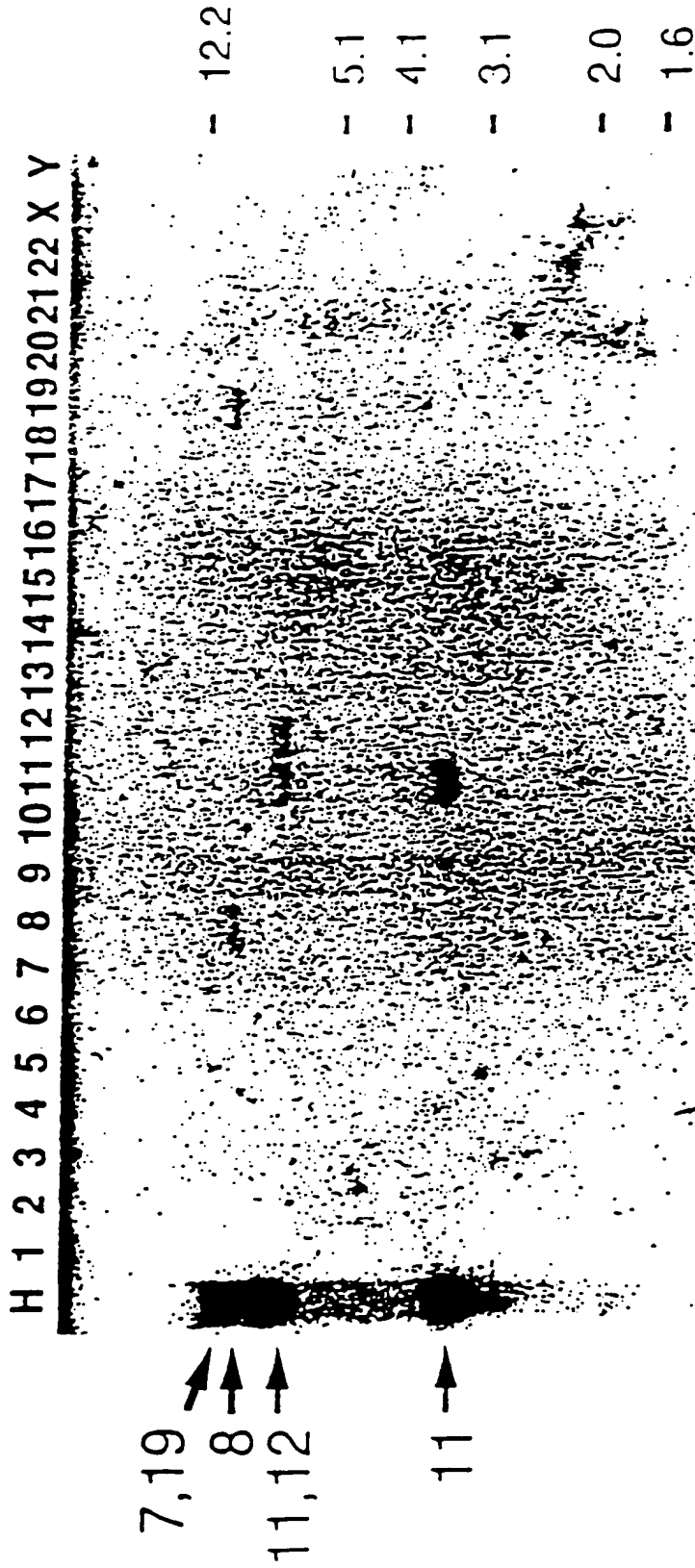


Fig. 21

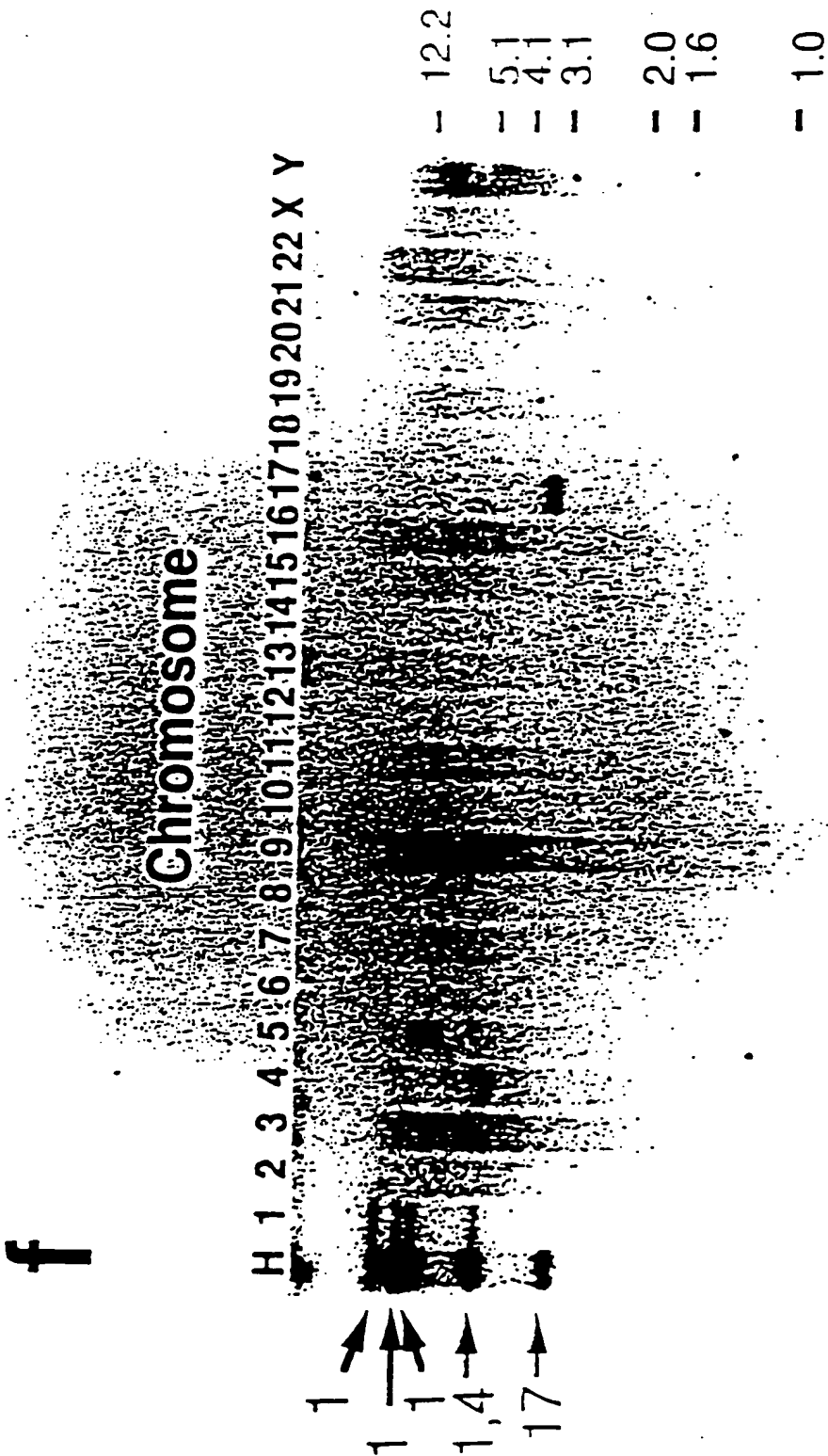


Fig. 22

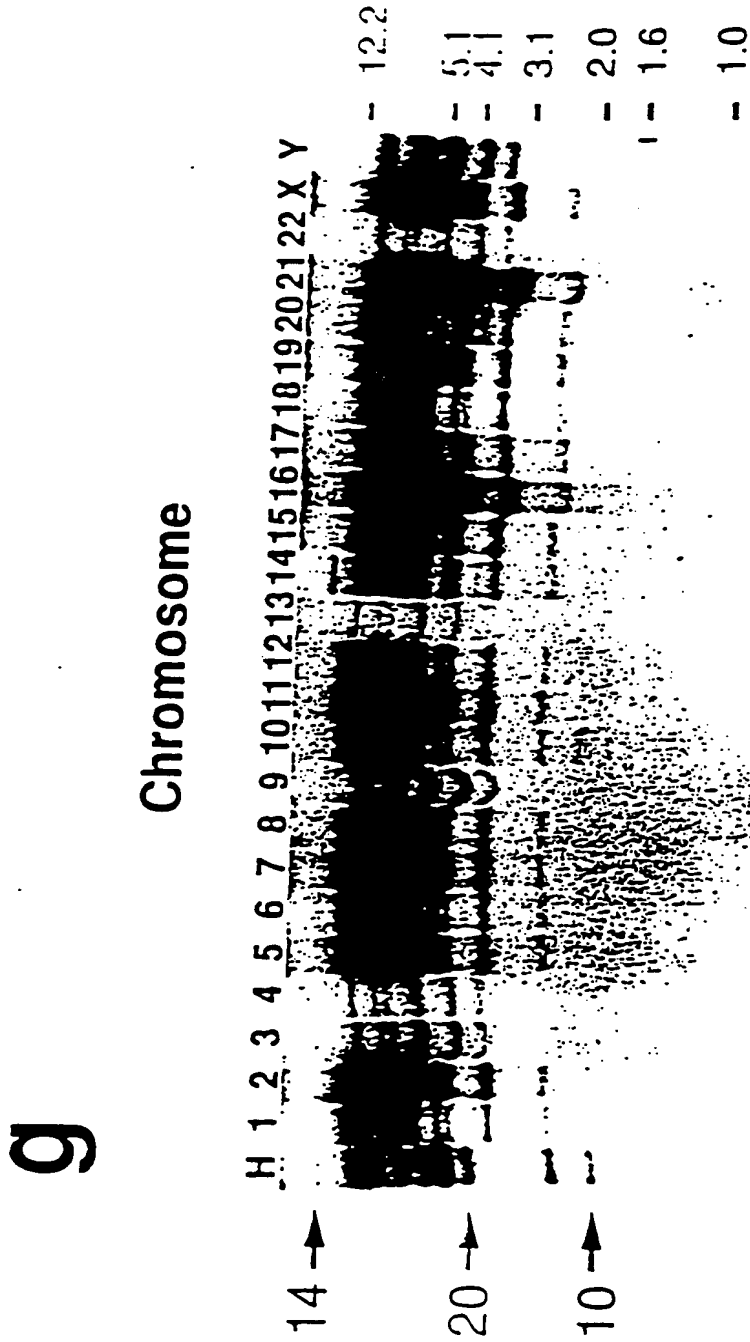


Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Numbers of bands detected with human whole chromosomes		Chromosomes assigned						Background	
Clone	Sequence length ±	2/3	3/3	3/3	3/3	3/3		Mouse	Chinese hamster
Single band group:									
c12c11	GS000075	432	1	1	1	1	9	0	0
c12c06	GS000062	540	1	1	1	1	6.15	0	0
c12g01	GS000290	212	1	1	1	1	2	1	1
c13c05	GS000117	359	1	1	1	1	11-	0	0
c13c07	GS000120	355	1	1	1	1	2	0	0
c13f10	GS000206	267	1	1	1	1	14	0	0
c13h01	GS000279	133	1	1	1	1	12-	0	0
c13h02	GS000322	167	1	1	1	1	6	0	0
d0g02	GS000095	397	1	1	1	1	3	0	0
d0h07	GS000134	313	1	1	1	1	11	1	1
d1b10	GS000344	151	1	1	1	1	20	0	0
hm01c12	GS000223	246	1	1	1	1	27	0	0
hm01c09	GS000423	157	0	1	1	1	1	0	0
hm01c12	junk	394	1	1	1	1	17	0	0
hm01f05	GS000066	454	1	1	1	1	19.22	0	0
hm01f10	GS000299	173	0	1	1	1	10	0	0
hm01g09	GS000053	477	1	1	1	1	6	0	0
hm01h07	GS000115	363	1	1	1	1	12	0	0
hm02a02	GS000130	344	1	1	1	1	4	0	0
hm02a04	GS000329	164	1	1	0	0	10	0	0
hm02c01	GS000293	271	1	1	1	1	16	0	0
hm02c01	GS000015	590	1	1	1	1	20	0	0
hm02c02	GS000342	156	0	1	1	1	14	0	0
hm02c05	GS000401	223	1	1	0	0	n.d.	0	0
hm02g02	GS000191	273	1	1	1	1	17	0	0
hm05c05	GS000251	219	1	1	1	1	6	2	0
hm05a10	junk	392	1	1	1	1	1	1	1
hm05c10	GS000009	606	1	1	1	1	1	0	0
kmc01	junk	169	1	1	1	0	n.d.	0	0
s105	GS000001	703	1	1	1	1	5	0	0
s110	GS000057	471	1	1	1	1	3	0	0
s11d11	GS000307	#175	0	0	0	1	7	0	0
s11h01	GS000259	204	1	1	1	1	3	0	0
s147	GS000050	461	1	1	1	0	2	0	0
s14c06	junk	619	1	1	1	1	1	0	0
s14g02	GS000132	322	1	1	1	1	4	0	0
s14h12	GS000271	193	1	1	1	1	4	1	1
s150	GS000143	330	1	1	1	1	17	0	0
s156	GS000002	306	1	1	1	1	2	1	1
s15b11	GS000250	221	1	1	1	1	14	0	0
s179	GS000275	196	1	1	1	1	n.d.	0	0
s246	GS000224	241	1	1	1	1	9	0	0
s247	GS000347	153	1	1	1	1	1	0	0
s270	junk	135	1	1	1	1	19	0	0

Fig. 24

Numbers of bands detected with human whole chromosomes			Chromosomes assigned					Background	
Clone	Sequence length	Σ	$\Sigma/91$	$\Sigma/35$	$31/35$		Mouse	Chinese hamster	
s306	CS000256	203	1	1	0	1	X	0	0
s309	CS000171	303	1	1	0	1	1	0	0
s342	CS000323	163	1	1	1	1	4	3	2
s331	CS000255	207	1	1	0	1	6.13	1	1
s334	CS000165	312	1	1	1	1	1	0	0
s337	CS000276	193	1	1	1	1	17	0	0
s339	CS000295	130	1	1	1	1	n.d.	0	1
s443	CS000330	231	1	1	1	1	n.d.	0	0
s470	junk	251	1	1	1	1	17	0	0
s474	CS000192	273	1	1	1	1	3	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	CS000334	141	1	1	1	1	14	1	1
s632	junk	387	1	1	1	1	2	0	0
s633	CS000166	311	1	1	1	1	22	2	1
s650	CS000041	644	1	1	1	1	12	1	1
tw1-04	CS000025	537	1	1	1	1	3.7	0	0
tw1-19	CS000218	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	CS000237	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	8	1	1
tw1-48	CS000098	178	1	1	1	1	14	0	0
tw1-96	CS000138	339	1	1	1	1	11	0	0
Two band group:									
e12212	CS000195	277	1	2	2	2	1.	1	1
e13402	CS000042	503	2	2	1	1	2.	0	0
hm01a06	CS000129	344	2	2	2	2	11.13	3	3
hm01a07	CS000207	249	2	2	2	2	7.	0	0
hm01d05	CS000232	243	2	2	2	1	2.	0	0
hm01e01	CS000181	292	2	2	2	2	1.2	0	0
hm02a08	CS000435	302	2	2	2	2	3.	1	1
hm02e04	CS000221	253	2	2	2	2	3.	0	0
hm02e05	CS000146	332	2	2	2	2	17.19.22	0	0
hm03f07	CS000043	303	1	1	2	1	3.	0	0
s11d06	CS000268	203	2	2	2	2	11.12	0	0
s11g12	CS000337	233	2	2	2	2	6.	0	0
s124	CS000088	404	2	2	2	2	9.	1	1
s144	CS000132	342	1	2	2	2	1.7	0	0
s14f03	CS000239	243	1	2	2	2	2.	3	2
s15e02	junk	439	2	2	1	2	6.	0	0
s16b09	junk	420	1	1	1	2	10.14	0	0
s17e09	CS000248	223	2	2	2	2	14.	0	0
s231	junk	284	2	2	2	2	11.	0	0
s234	CS000124	353	2	2	2	2	1.	3	1
s253	CS000235	219	2	2	2	2	11.	0	0
s272	junk	193	2	2	2	2	10.16	1	1

Fig. 25

Numbers of bands detected with human whole chromosomes			Chromosomes assigned				Background	
Clone	Sequence length	5	E/5: 3/5: 3/5:	5	3/5: 3/5:		Mouse	Chinese hamster
s311	CS000092	333	1	1	2	2	16.	1
s313	junk	132	2	2	1	0	20.	0
s317	CS000100	339	0	0	1	2	14,14	1
s336	CS000134	337	2	2	2	2	12,14	0
s333	CS000139	233	2	2	2	1	22,X	0
s339	CS000233	737	2	1	1	2	17.	0
s394	CS000063	449	2	1	2	2	13,14	0
s396	junk	277	2	2	2	2	17.	0
s455	junk	452	1	2	2	1	4.	0
s456	CS000236	132	2	2	2	2	8,10	1
s465	CS000201	374	1	1	2	2	6,15	0
s615	junk	250	1	1	1	2	9,13	0
s639	CS000257	205	1	2	2	2	2X	0
s656	CS000025	590	2	2	0	2	6,11	0
twl-33	junk	352	2	2	2	2	1.	0
twl-39	CS000153	321	2	2	2	2	17.	0
twl-70	CS000061	441	1	1	2	1	11.	0
twl-80	junk	453	2	2	1	2	9,17	2
twl-87	CS000152	316	2	2	2	2	7.	0
Three band group								
d0h06	CS000030	417	3	3	3	1	1.	0
hm05b07	junk	336	2	3	3	3	5.	0
hm05g02	CS000209	267	2	2	2	1	3,17,19	1
s129	CS000107	373	3	3	3	3	n.d.	1
s173	CS000357	146	1	2	2	3	2.	0
s17a10	CS000294	131	3	3	3	3	2,13,22	1
s308	CS000412	638	2	2	2	3	XX	1
s401	CS000224	249	2	3	3	3	6,6.	0
s654	CS000045	491	3	3	3	3	1,22.	0
twl-82	CS000202	267	3	3	3	3	13.	4
Four band group								
cl2g07	CS000154	320	4	4	2	3	5, 14.	0
cl3a08	CS000055	508	3	3	4	4	2,7,7,17	1
cl3c04	CS000106	376	4	3	3	3	n.d.	0
cl3c09	CS000302	195	4	2	4	4	2,17.	7
s136	CS000160	315	4	4	4	4	4X	2
s163	CS000004	618	4	4	4	2	4,4,8,20	3
s479	CS000130	293	4	4	2	2	7,3,11,11,12,19	0
Group with 5 or more bands								
cl2f08	CS000253	217	5	5	5	2	2,7,9,14.	2
hc01	junk	374	12	12	13	13	1,2,6.	22
hd10	junk	361	4	4	4	8	n.d.	12
he10	junk	173	6	2	3	3	6,3,9,19,21.	3
hm01c05	CS000205	176	9	7	5	5	X	9
hm01f04	CS000246	215	8	10	5	5	n.d.	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14

Fig. 26

Numbers of bands detected with human whole chromosomes				Chromosomes assigned			Background		
Clone	Sequence length	≡	≡/3 ₁	≡/3 ₂	≡/3 ₃		Mouse	Chinese hamster	
hm02f09	CS000273	442	3	7	7	5	3,3,6,11,13,14,15,16	0	0
hm03a02	CS000096	373	5	6	4	6	2,3,17.	3	3
hm03a04	CS000236	239	6	6	6	7	n.d.	2	5
km501	junk	350	3	5	5	5	13.	14	7
s11f06	CS000316	170	6	6	6	4	1,2,2,3,4,6,13,15.	0	3
s14f01	CS000407	252	12	11	10	9	1,5,9,13.	6	3
s175	CS000094	397	5	4	4	3	1,1,1,1,4,17	0	0
s265	CS000323	167	10	12	11	14	13.	9	5
s341	junk	494	9	9	8	6	n.d.	15	3
s406	CS000113	364	6	7	5	4	2,7,8,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X.	3	5
tw1-63	junk	203	3	10	10	12	3,4.	17	11
Bands no detected:									
cl3g02	CS000340	157	0	0	0	0	-	-	-
hm01e10	junk	232	0	0	0	0	-	-	-
hm02d11	CS000274	196	0	0	0	0	-	-	-
s323	CS000273	194	0	0	0	0	-	-	-
s359	CS000199	279	0	0	0	0	-	-	-
s511	junk	235	0	0	0	0	-	-	-
s645	CS000012	2734	0	0	0	0	-	-	-
s647	CS000105	360	0	0	0	0	-	-	-
s651	junk	540	0	0	0	0	-	-	-

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl⁶ C12N15/11, C12Q1/68//G01N33/566

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int. Cl⁶ C12N15/11, C12Q1/68//G01N33/566

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

BIOSIS PREVIEWS, CAS ONLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids. Res., Vol. 15, 1987, Ou, J. H. "Cloning and characterization of a human ribosomal protein gene with enhanced expression in fetal and neoplastic cells" p. 8919-8934	1-6 (164)
X	Differentiation, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
X	J. Biol. Chem., Vol. 265, 1990, Wilkin, D. J. et al. "Isolation and sequence of the human farnesyl pyrophosphate synthetase cDNA: coordinate regulation of the mRNAs for farnesyl pyrophosphate synthetase, 3-hydroxy-3-methylglutaryl coenzyme A reductase, and 3-hydroxy-3-methylglutaryl coenzyme A synthetase" p. 4607-4614	1-6 (255)

☒ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

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"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"Z" document member of the same patent family

Date of the actual completion of the international search

February 6, 1995 (06. 02. 95)

Date of mailing of the international search report

March 7, 1995 (07. 03. 95)

Name and mailing address of the ISA/

Japanese Patent Office

Facsimile No.

Authorized officer

Telephone No.

INTERNATIONAL SEARCH REPORT

International application No.

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C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Batra, S. K. et al. "Molecular cloning and sequence analysis of the human ribosomal protein S16" p. 6830-6833	1-6 (275)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Ben-Ishai, R. et al. "A human cellular-sequence implicated in trk oncogene activation is DNA damage inducible" p. 6039-6043	1-6 (313)
X	J. Biol. Chem., Vol. 263, 1988, Fischer, R. et al. "Multiple divergent mRNAs code for a single human calmodulin" p. 17055-17062	1-6 (386)
X	J. Cell Biol., Vol. 108, 1989, Barnett, T. R. et al. "Carcinoembryonic antigens: Alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic antigen family" p. 267-276	1-6 (446)
X	J. Biol. Chem., Vol. 265, 1990, Natsumeda, Y. et al. "Two distinct cDNAs for human IMP dehydrogenase" p. 5292-5295	1-6 (454)
X	Genes Dev., Vol. 7, 1993, Patton, J. G. et al. "Cloning and characterization of PSF a novel pre-mRNA splicing factor" p. 393-406	1-6 (706)
X	Nucleic Acids Res., Vol. 16, 1988, Stanford, D. R. et al. "The complete primary structure of the human snRNP E protein" p. 10593-10605	1-6 (711)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 84, 1987, Inoue, C. et al. "Evolutionary conservation of the insulinoma gene rig and its possible function" p. 6659-6662	1-6 (723)
X	J. Immunol., Vol. 144, 1990, Jongstra-Bilen, J. et al. "Human and mouse LSP1 genes code for highly conserved phosphoproteins" p. 1104-1110	1-6 (741)
X	Biochem. J., Vol. 248, 1987, Sakai, I. et al. "The cDNA and protein sequences of human lactate dehydrogenase-B" p. 933-936	1-6 (772)

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Biochim. Biophys. Acta., Vol. 1089, 1991, Tamura, T. et al. "Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multicatalytic proteinase complexes)" p. 95-102	1-6 (775)
X	Mol. Cell. Biol., Vol. 3, 1983, Cowan, N. J. et al. "Expression of human alpha-tubulin genes: interspecies conservation of 3' untranslated regions" p. 1738-1745	1-6 (820)
X	Nucleic Acids Res., Vol. 17, 1989, Taaman, J. W. et al. "Nucleotide sequence of cDNA encoding subunit VIb of human cytochrome c oxidase" p. 1766-1766	1-6 (844)
X	Gene, Vol. 93, 1990 Taanman, J. W., Schrage, C., Ponne, N., Das, A., Bolhuis, P. A., de Vries, H. and Agsteribbe, E. Isolation of cDNAs encoding Subunit VIb of human cytochrome c oxidase and steady-state levels of coxVIb mRNA in different tissues p. 285-291	1-6 (844)
X	J. Biol. Chem., Vol. 264, 1989, Gray, P. W. et al. "Cloning of the cDNA of a human neutrophil bactericidal protein: Structural and functional correlations" p. 9505-9509	1-6 (861)
X	Immunogenetics, Vol. 32, 1990, Angelisova, P. et al. "The human leucocyte surface antigen CD53 is a protein structurally similar to the CD37 and MRC OX-44 antigens" p. 281-285	1-6 (1158)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 88, 1991, Koken, M. H. et al. "Structural and functional conservation of two human homologs of the yeast DNA repair gene RAD6" p. 8865-8869	1-6 (1181)
X	Oncogene, Vol. 5, 1990, Firnbach-Kraft, I. et al. "Tyk 2, prototype of a novel class of non-receptor tyrosine Kinase genes" p. 1329-1336	1-6 (1345)
X	Science, Vol. 248, 1990, Smith, C. A. et al. "A receptor for human tumor necrosis factor defines an unusual family of cellular and viral proteins" p. 1019-1023	1-6 (1431)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 263, 1988, Luster, A. D. et al. "Molecular and biochemical characterization of a novel gamma-interferon-inducible protein" p. 12036-12043	1-6 (1455)
X	J. Clin. Invest., Vol. 83, 1989, Look, A. T. et al. "The human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminopeptidase N" p. 1299-1307	1-6 (1469)
X	J. Cell Biol., Vol. 105, 1987, Argraves, W. S. et al. "Amino Acid Sequence of the Human Fibronectin Receptor" p. 1183-1190	1-6 (1607)
X	Nucleic Acids Res., Vol. 18, 1990, Liebhaber, S. A. et al. "Characterization of a human cDNA encoding a widely expressed and highly conserved cysteine-rich protein with an unusual zinc-finger motif" p. 3871-3879	1-6 (1642)
X	J. Biol. Chem., Vol. 264, 1989, Didsbury, J. et al. "Rac, a novel ras-related family of proteins that are bolulinum toxin substrates" p. 16378-16382	1-6 (1709)
X	EMBO J., Vol. 6, 1987, Willison, K. et al. "The human homologue of the mouse t-complex gene, TCPI, is located on chromosome 6 but is not near the HLA region" p. 1967-1974	1-6 (1749)
X	J. Biol. Chem., Vol. 266, 1991, Wu, Y. et al. "Activation of globin gene expression by cDNAs from induced K562 cells: Evidence for involvement of ferritin in globin gene expression" p. 17566-17572	1-6 (1785)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ikuta, T. et al. "Three human alcohol dehydrogenase subunits: cDNA structure and molecular and evolutionary divergence" p. 634-638	1-6 (1864)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 85, 1988, Fukumoto, H. et al. "Sequence, tissue distribution, and chromosomal localization of mRNA encoding a human glucose transporter-like protein" p. 5434-5438	1-6 (1878)

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International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Clin. Invest., Vol. 76, 1985, Cooke, N.E. et al. "Serum vitamin D-binding protein is a third member of the albumin and alpha fetoprotein gene family" p. 2420-2424	1-6 (1888)
X	J. Biol. Chem., Vol. 264, 1989, Huang, S.-H. et al. "Human deoxycytidine kinase: Sequence of cDNA clones and analysis of expression in cell lines with and without enzyme activity" p. 14762-14768	1-6 (1894)
X	J. Biol. Chem., Vol. 266, 1991, Huang, S.-H. et al. "Additions and corrections Human deoxycytidine kinase. Sequence of cDNA clones and analysis of expression in cell lines with and without anzyme activity" p. 5353-5353	1-6 (1894)
X	Somat. Cell Mol. Genet., Vol. 11, 1985, Bell, G.I. et al. "Human alpha-2-macroglobulin gene is located on chromosome 12" p. 285-289	1-6 (1895)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 81, 1984, Yang, F. et al. "Human transferrin: cDNA characterization and chromosomal localization" p. 2752-2756	1-6 (1902)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ny, T. et al. "Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor" p. 6776-6780	1-6 (1904)
X	J. Biol. Chem., Vol. 267, 1992, Bausch-Jurken, M. T. et al. "Molecular cloning of AMP deaminase isoform L: Sequence and bacterial expression of human AMPD2 cDNA" p. 22407-22413	1-6 (1908)
X	Gene, Vol. 44, 1986, Board, P. G. et al. "Molecular cloning and nucleotide sequence of human alpha-1 acid glycoprotein cDNA" p. 127-131	1-6 (1921)
X	Eur. J. Biochem., Vol. 155, 1986, Wathelet, M. et al. "Molecular cloning, full-length sequence and preliminary characterization of a 56-kDa protein induced by human interferons" p. 11-17	1-6 (2101)

INTERNATIONAL SEARCH REPORT

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PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^o	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids Res., Vol. 11, 1983, Chebath, J. et al. "Interferon induced 56,000 mr protein and its mRNA in human cells: molecular cloning and partial sequence of the cDNA" p. 1213-1226	1-6 (2101)
X	Biochemistry, Vol. 25, 1986, Koide, T. et al. "Amino acid sequence of human histidine-rich glycoprotein derived from the nucleotide sequence of its cDNA" p. 2220-2225	1-6 (2174)
X	Biochemistry, Vol. 22, 1983, Friezner-Degen, S. J. et al. "Characterization of the complementary deoxyribonucleic acid and gene coding for human prothrombin" p. 2087-2097	1-6 (2214)
X	Biochem. J., Vol. 268, 1990, Steinkasserer, A. et al. "Heterogeneity in human serum amyloid A protein. Five different variants from one individual demonstrated by cDNA sequence analysis." p. 287-193	1-6 (2238)
X	Nucleic Acids Res., Vol. 17, 1989, Fabrizi, G. M. et al. "Sequence of a cDNA specifying subunit VIIa of human cytochrome c oxidase" p. 7107-7107	1-6 (2264)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 86, 1989, Sims, J. E. et al. "Cloning of the interleukin 1 receptor from human T cells" p. 8946-8950	1-6 (2265)
X	Eur. J. Biochem., Vol. 169, 1987, Mackinnon, C. M. et al. "Molecular cloning of cDNA for human complement component C1s. The complete amino acid sequence" p. 547-553	1-6 (2266)
X	J. Virol., Vol. 65, 1990, Tsujimoto, A. et al. "Isolation of cDNA for DNA binding proteins which specifically bind to TAX-responsive enhancer element in the LTR of HTLA-1" p. 1420-1426	1-6 (2475)
X	Immunogenetics, Vol. 37, 1993, Emi, N. et al. "Isolation of a novel cDNA clone showing marked similarity to ME491/CD63 superfamily" p. 193-198	1-6 (2556)
X	Nature, Vol. 353, 1991, Kelly, A. P. et al. "A new human HLA class II-related locus, DM" p. 571-573	1-6 (2583)

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International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 265, 1990, Hla, T. et al. "An abundant transcript induced in differentiating human endothelial cells encodes a polypeptide with structural similarities to G-protein-coupled receptors" p. 9308-9313	1-6 (2600)
X	J. Biol. Chem., Vol. 267, 1992, White, R. T. et al. "Human adipsin is identical to complement factor D and expressed at high levels in adipose tissue" p. 9210-9213	1-6 (2802)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Rouault, T. A. et al. "Cloning of the cDNA encoding RNA regulatory protein-the human iron-responsive element-binding protein" p. 7958-7962	1-6 (2832)
X	Nucleic Acids Res., Vol. 17, 1989, Sawada, R. et al. "Complementary DNA sequence and deduced peptide sequence for CD59/MEM43 antigen, the human homologue of murine lymphocyte antigen Ly-6c" p. 6728-6728	1-6 (2954)
X	DNA Cell Biol., Vol. 9, 1990, Sawada, R. et al. "Isolation and expression of the full-length cDNA encoding CD59 antigen of human lymphocytes" p. 213-220	1-6 (2954)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Weller, P. A. et al. "Complete sequence of human vinculin and assignment of the gene to chromosome 10" p. 5667-5671	1-6 (2983)
X	Cell, Vol. 58, 1989, Mellentin, J. D. et al. "LYL-1, a novel gene involved by chromosomal translocation in T-cell leukemia, codes for a protein with a helix-loop-helix DNA binding motif" p. 77-83	1-6 (3023)
X	Cell, Vol. 60, 1990, Uze, G. et al. "Genetic transfer of a functional human interferon alpha receptor into mouse cells: Cloning and expression of its cDNA" p. 225-234	1-6 (3041)
X	Biochem. Biophys. Res. Commun., Vol. 179, 1991, Xiao, L. et al. "Characterization of a full length cDNA which codes for the human spermidine/spermine N-1-acetyltransferase" p. 407-415	1-6 (3053)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^o	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Casero, R. A. Jr. et al. "Isolation and characterization of a cDNA clone that codes for human spermidine/spermine N-1-acetyltransferase" p. 810-814	1-6 (3053)
X	Nucleic Acids Res., Vol. 20, 1992, Wintzerith, M. et al. "Sequence of the human RNA polymerase II largest subunit" p. 910-910	1-6 (3083)
X	J. Cell Biol., Vol. 103, 1986, Lawler, J. et al. "The Structure of Human Thrombospondin, an/ adhesive Glycoprotein with Multiple Calcium binding Sites and Homologies with Several Different Proteins" p. 1635-1648	1-6 (3266)
X	Nature, Vol. 352, 1991, Maslen, C. L. et al. "Partial sequence of a candidate gene for the marfan syndrome" p. 334-337	1-6 (3334)
X	J. Cell Biol., Vol. 111, 1990, Fishman, G. I. et al. "Molecular Characterization and Functional Expression of the Human Cardiac Gap Junction Channel" p. 589-598	1-6 (3403)
X	Cell, Vol. 40, 1985, Ebina, Y. et al. "The human insulin receptor cDNA: The structural basis for hormone-activated membrane signalling" p. 747-758	1-6 (3447)
X	Oncogene, Vol. 5, 1990, Westin, E. H. et al. "Alternative splicing of the human c-myb gene" p. 1117-1124	1-6 (3529)
X	Genomics, Vol. 4, 1989, Todd, S. et al. "cDNA sequence, interspecies comparison and gene mapping analysis of argininosuccinate lyase" p. 53-59	1-6 (3575)
X	FEBS Lett., Vol. 207, 1986, Codina, J. et al. "-Subunits of the human liver Gs/Gi signal-transducing proteins and those of bovine retinal rod cell transducin are identical" p. 187-192	1-6 (3796)
X	Nucleic Acids Res., Vol. 18, 1990, Roessler, B. J. et al. "Cloning of two distinct copies of human phosphoribosyl pyrophosphate synthetase cDNA" p. 193-193	1-6 (3828)

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

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International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biochem., Vol. 109, 1991, Sonoda, T. et. al. "Complete nucleotide sequence of human phosphoribosyl pyrophosphate synthetase subunit I (PRS I) cDNA and a comparison with human and rat PRPS gene families" p. 361-364	1-6 (3828)
X	J. Biol. Chem., Vol. 263, 1988, Wermuth, B. et al. "Human carbonyl reductase: Nucleotide sequence analysis of a cDNA and amino acid sequence of the encoded protein" p. 16185-16188	1-6 (4033)
X	Biochim. Biophys. Acta. Vol. 1048, 1990, Forrest, G. L. et al. "Induction of a human carbonyl reductase gene located on chromosome 21" p. 149-155	1-6 (4033)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 88, 1991, Schuetz, T. J. et al. "Isolation of a cDNA for HSF2: Evidence for two heat shock factor genes in humans" p. 6911-6915	1-6 (4093)
X	Nucleic Acids Res., Vol. 13, 1985, Hallewell, R. A. et al. "Human Cu/Zn superoxide dismutase cDNA: isolation of clones synthesising high levels of active or inactive enzyme from an expression library" p. 2017-2034	1-6 (4110)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 80, 1983, Sherman, L. et al. "Nucleotide sequence and expression of human chromosome 21 - encoded superoxide dismutase mRNA" p. 5465-5469	1-6 (4110)
X	J. Biol. Chem., Vol. 268, 1993, David, V. et al. "Interaction with newly synthesized and retained proteins in the endoplasmic reticulum suggests a chaperone function for human integral membrane protein IP90 (calnexin)" p. 9585-9592	1-6 (4373)
X	J. Exp. Med., Vol. 172, 1990, Tekamp-Olson, P. et al. "Cloning and Characterization of cDNAs for Murine Macrophage Inflammatory Protein 2 and its Human Homologues" p. 911-919	1-6 (4452)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Biochemistry, Vol. 30, 1991, Tomkinson, B. et al. "Characterization of cDNA for human tripeptidyl peptidase II: The N-terminal part of the enzyme is similar to subtilisin" p. 168-174	1-6 (4522)
X	J. Biol. Chem., Vol. 263, 1988, Verma, A. K. et al. "Complete primary structure of a human plasma membrane Ca ²⁺ pump" p. 14152-14159	1-6 (4673)
X	J. Biol. Chem., Vol. 267, 1992, Shechter, I. et al. "Solubilization, purification and characterization of a truncated form of rat hepatic squalene synthetase" p. 8628-8635	1-6 (4818)
X	J. Biol. Chem., Vol. 267, 1992, McKenzie, T. L. et al. "Molecular cloning, expression, and characterization of the cDNA for the rat hepatic squalene synthase" p. 21368-21374	1-6 (4818)
X	Nucleic Acids Res., Vol. 13, 1985, Furutani, Y. et al. "Cloning and characterization of the cDNAs for human and rabbit interleukin-1 precursor" p. 5869-5882	1-6 (4872)
X	Proc. Natl. Acad. Sci U.S.A., Vol. 89, 1992, Katoh, M. et al. "K-sam gene encodes secreted as well as transmembrane receptor tyrosine kinase" p. 2960-2964	1-6 (4914)
X	Differentiation, Vol. 42, 1989, Kuruc, N. et al. "Synthesis of cytokeratin 13, a component characteristic of internal stratified epithelia, is not induced in human epidermal tumors" p. 111-123	1-6 (5264)
X	J. Biol. Chem., Vol. 266, 1991, Kiefer, M. C. et al. "Identification and molecular cloning of two new 30-kDa insulin-like growth factor binding proteins isolated from adult human serum" p. 9043-9049	1-6 (5374)

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INTERNATIONAL SEARCH REPORT

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C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 265, 1990, Opipari, A. W. et al. "The A20 cDNA induced by tumor necrosis factor alpha-encodes a novel type of zinc finger protein" p. 14705-14708	1-6 (5427)
X	J. Biol. Chem., Vol. 265, 1990, McLean, J. W. et al. "cDNA sequence of the human integrin beta-5 subunit" p. 17126-17131	1-6 (5715)
X	Cell, Vol. 66, 1991, Ge, H. et al. "primary structure of the human splicing factor ASF reveals similarities with drosophila regulators" p. 373-382	1-6 (5860)
X	Cancer Res., Vol. 52, 1992, Kondoh, N. et al. "Differential expression of S19 ribosomal protein, laminin binding protein and HLA class I mRNAs associated with colon carcinoma progression and differentiation" p. 791-796	1-6 (6439)
X	J. Biol. Chem., Vol. 263, 1988, Collart, F. R. et al. "Cloning and sequence analysis of the human and chinese hamster inosine-5' -monophosphate dehydrogenase cDNA" p. 15769-15772	1-6 (6471)
X	J. Biol. Chem., Vol. 261, 1986, Romeo, P. -H. et al. "Molecular cloning and nucleotide sequence of a complete human uroporphyrinogen decarboxylase cDNA" p. 9825-9831	1-6 (6569)
X	J. Cell Biol., Vol. 106, 1988, Leube, R. E. et al. "Molecular characterization and expression of the stratification-related cytokeratins 4 and 15" p. 1249-1261	1-6 (6875)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 85, 1988, Daher, K. A. et al. "Isolation and characterization of human defensin cDNA clones" p. 7327-7331	1-6 (7106)
X	J. Exp. Med, Vol. 172, 1990, Larsen, A. et al. "Expression Cloning of a Human Granulocyte Colony-stimulating Factor Receptor: a Structural Mosaic of Hematopoietin Receptor, Immunoglobulin, and Fibronectin Domains" p. 1559-1570	1-6 (7126)

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International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Oncogene, Vol. 8, 1993, Schulz, A. S. et al. "The genomic structure of the human UFO receptor" p. 509-513	1-6 (7790)
A	Nature Genetics, Vol. 2, 1992, Okubo, K. et al. "Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression" p. 173-179	1-6 --
A	Nature Genetics, Vol. 2, 1992, Khan, A. S. et al. "Single pass sequencing and physical and genetic mapping of human brain cDNAs" p. 180-188	1-6

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